



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 178125**

**TO: Ruixiang Li**  
**Location: REM/4D75/4C70**  
**Art Unit: 1646**  
**Friday, November 25, 2005**  
**Case Serial Number: 09/475158**

**From: Toby Port**  
**Location: Biotech-Chem Library**  
**REM-1A59**  
**Phone: 571-272-2523**  
**toby.port@uspto.gov**

### **Search Notes**

**Examiner Li,**

**See attached results.**

**If you have any questions about this search feel free to contact me at any time.**

**Thank you for using STIC search services!**

**Toby Port**  
**X22523**

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STIC-Biotech/ChemLib

170128

From: Li, Ruixiang  
Sent: Monday, October 31, 2005 2:39 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search of Application No.09/475,158

Please do a standard search on:

- (i).SEQ ID NOS: 3 and 5 against both commercial and interference amino acid databases;
- (ii). SEQ ID NOS: 14, 15, and 16 against both commercial and interference nucleic acid databases;
- (iii). AlaValSerGluIleGlnLeuMetHisAsnLeuGlyGlyGlyGlyGly against both commercial and interference amino acid databases.

Thank you very much!

Ruixiang Li  
GAU 1646  
REM 4D75  
Mail Box 4C70  
(571) 272-0875

RECEIVED  
OCT 31 2005  
STIC-BIOTECH/CHEM LIBRARY  
(STIC)

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2005, 15:52:37 ; Search time 141.5 Seconds  
(without alignments)  
96.260 Million cell updates/sec

Title: US-09-475-158A-3

Perfect score: 160

Sequence: 1 AVSEIQLMHGGGGGLNSMERVEWLKRLQDV 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq 21.\*

1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	160	100.0	31	AAy96973	Parathyro
2	146	91.2	31	AAy96975	Parathyro
3	133	83.1	38	Aar58104	[Gly13]-h
4	129	80.6	34	Aar22294	Human par
5	129	80.6	35	Aar74462	Parathyro
6	129	80.6	36	Aar58271	[Ala11]-h
7	128	80.0	33	AAy98015	Human ami
8	128	80.0	34	AAW17941	Human par
9	128	80.0	34	AAW67276	Parathyro
10	128	80.0	34	AAy98014	Human ami
11	128	80.0	36	Aar58248	N-Dimethy
12	128	80.0	36	Aar58026	N-alpha-m
13	128	80.0	36	Aar58262	[Ala1]-hp
14	128	80.0	38	Aar58019	N-alpha-m
15	127	79.4	31	AAy96974	Parathyro
16	127	79.4	34	Aar22296	Human par
17	127	79.4	34	AAW08117	Human PTH
18	127	79.4	34	Aau73030	Parathyro
19	127	79.4	34	AAU73029	Parathyro
20	127	79.4	34	ADQ75344	PTH/PTHrP
21	127	79.4	34	ADQ75345	PTH/PTHrP
22	127	79.4	35	Aar74466	Parathyro
23	127	79.4	35	AAr74470	Parathyro
24	127	79.4	35	AAU73173	Parathyro

25	127	79.4	35	8	ADQ75490	Adq75490 PTH/PTHrP
26	127	79.4	35	8	ADQ75489	PTH/PTHrP
27	127	79.4	36	2	Aar58209	[Ala14]-h
28	127	79.4	36	2	Aar58207	[Ala13]-h
29	127	79.4	38	2	Aar58024	[Ala1,11e
30	127	79.4	38	2	Aar58037	[Ser14]-h
31	127	79.4	38	2	Aar58093	[Asn13]-h
32	127	79.4	38	2	Aar58098	[Ser13]-h
33	127	79.4	38	2	Aar58103	[Ala13]-h
34	127	79.4	38	2	Aar58106	[Ala14]-h
35	126	78.8	31	9	ADW95207	Aad95207 Amino aci
36	126	78.8	31	9	ADW95208	Amino aci
37	126	78.8	34	2	AAW22292	Human par
38	126	78.8	34	2	AAW08108	Human par
39	126	78.8	38	2	Aar58095	[Asp13]-h
40	125	78.1	31	2	AAW42059	Human par
41	125	78.1	31	2	AAW42051	Human par
42	125	78.1	31	2	AAy02578	N-termina
43	125	78.1	31	4	AAW81080	Human par
44	125	78.1	31	4	AAW91097	Parathyro
45	125	78.1	31	5	AAE23720	Human par

#### ALIGNMENTS

RESULT 1  
AAy96973  
ID AAy96973 standard; peptide; 31 AA.  
XX AC AAy96973;  
XX DT 31-OCT-2000 (first entry)  
XX DE Parathyroid hormone functional domain conjugate peptide PG5.  
XX KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;  
KW resorption; remodeling; tether1; osteoporosis.  
XX OS Homo sapiens.  
OS Synthetic.  
XX FH Key  
FT Peptide  
FT /label= PTH N-terminal\_signaling\_domain  
FT /note= "residues 1-9"  
FT Peptide  
FT /label= linker  
FT /label= linker  
FT Peptide  
FT /label= PTH C-terminal\_binding\_portion  
FT /note= "residues 15-31"  
XX WO200039278-A2.  
XX 06-JUL-2000.  
XX 30-DEC-1999; 99WO-US031108.  
XX 31-DEC-1998; 98US-0114577P.  
XX (GARD//) GARDELLA T J.  
XX (KRON//) KRONENBERG H M.  
XX (POTT//) POTTS J T.  
XX (JUEP//) JUEPPNER H.  
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
XX WPI: 2000-452384/39.  
XX N-PSDB; AA51729.  
XX New compound comprising an amino terminal signaling functional domain  
XX linked to a carboxy-terminal binding portion of parathyroid hormone for  
XX treating mammalian conditions characterized by decreases in bone mass.

XX  
PS Claim 7; Page 92-93; 119pp; English.  
XX  
CC Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n  
CC -R- are new. S is an amino terminal signaling functional domain of  
CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the  
CC PTH-1 receptor signal sequence; and R 2 is (a portion of) PTH-1 receptor  
CC sequence. The new compounds are used for treating mammalian conditions  
CC characterized by decreases in bone mass, determining rates of bone  
CC reformation, bone resorption and/or bone remodeling, treating diseases  
CC and disorders associated with decreased tether activity, increasing CAMP  
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
CC non-peptide PTH (claimed). The new compound can be administered by  
CC inhalation unlike the large native PTH or PTHrp which avoids the need for  
CC regular injections to treat osteoporosis  
XX  
SQ Sequence 31 AA;  
Query Match 100.0%; Score 160; DB 3; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.4e-14;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AVSEIQLMHGGGGGLNSMERVWLRLKKLQDV 31  
Db 1 AVSEIQLMHGGGGGLNSMERVWLRLKKLQDV 31  
RESULT 2  
AAI96975 standard; peptide; 31 AA.  
AC AAI96975;  
AC AAI96975;  
DT 31-OCT-2000 (first entry)  
XX  
DE Parathyroid hormone functional domain conjugate peptide PG7.  
XX  
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;  
KW resorption; remodeling; tether1; osteoporosis.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..9  
FT /label= PTH N-terminal\_signaling\_domain  
FT /note= "residues 1-9"  
FT Peptide 10..16  
FT /label= linker  
FT Peptide 17..31  
FT /label= PTH C-terminal\_binding\_portion  
FT /note= "residues 17-31"  
XX  
DN WO200039278-A2.  
XX  
XX 06-JUL-2000.  
PD  
PF 30-DEC-1999; 99WO-US031108.  
XX  
PR 31-DEC-1998; 98US-0114577P.  
XX  
XX (GARD/) GARDELLA T J.  
PA (KRON/) KRONENBERG H M.  
PA (POTT/) POTTS J T.  
PA (JUEP/) JUEPPNER H.  
XX  
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
PI WPI; 2000-452384/39.  
XX DR N-PSDB; AAA51730.  
XX

PT New compound comprising an amino terminal signaling functional domain  
PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
PT treating mammalian conditions characterized by decreases in bone mass.  
XX  
PS Claim 7; Page 93; 119pp; English.  
XX  
CC Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n  
CC -R- are new. S is an amino terminal signaling functional domain of  
CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the  
CC PTH-1 receptor signal sequence; and R 2 is (a portion of) PTH-1 receptor  
CC sequence. The new compounds are used for treating mammalian conditions  
CC characterized by decreases in bone mass, determining rates of bone  
CC reformation, bone resorption and/or bone remodeling, treating diseases  
CC and disorders associated with decreased tether activity, increasing CAMP  
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
CC non-peptide PTH (claimed). The new compound can be administered by  
CC inhalation unlike the large native PTH or PTHrp which avoids the need for  
CC regular injections to treat osteoporosis  
XX  
SQ Sequence 31 AA;  
Query Match 91.2%; Score 146; DB 3; Length 31;  
Best Local Similarity 93.5%; Pred. No. 1.2e-12;  
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AVSEIQLMHGGGGGLNSMERVWLRLKKLQDV 31  
Db 1 AVSEIQLMHGGGGGLNSMERVWLRLKKLQDV 31  
RESULT 3  
AAI96975 standard; peptide; 38 AA.  
AC AAI96975;  
AC AAI96975;  
DT 20-SEP-1994 (first entry)  
XX  
DE [Gly131]-hPTH(1-38)-OH.  
XX  
KW Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;  
KW fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.  
XX  
OS Synthetic.  
XX  
PN GB2269176-A.  
XX  
PD 02-FEB-1994.  
XX  
PF 12-JUL-1993; 93GB-00014384.  
XX  
PR 15-JUL-1992; 92GB-00015009.  
PR 18-DEC-1992; 92GB-00026415.  
PR 23-DEC-1992; 92GB-00026859.  
PR 23-DEC-1992; 92GB-00026861.  
PR 28-JAN-1993; 93GB-00001691.  
PR 28-JAN-1993; 93GB-00001692.  
PR 14-APR-1993; 93GB-00007673.  
PR 19-APR-1993; 93GB-00008033.  
XX  
DA (SANO ) SANDOZ LTD.  
XX  
XX Lewis I, Schneider H, Waelchli R, Rainer A;  
PI WPI; 1994-018352/03.  
XX  
DR WPI; 1994-018352/03.  
XX  
XX New active para-thyroid hormone variants - used for treating or  
PT preventing osteoporosis etc.  
XX  
XX Example 101; Page 39; 92pp; English.  
XX

RESULT 5  
AAR74462

```
DT 20-SEP-1994 (first entry)
DE [Ala11]-hPTH(1-36)-NH2.
DE Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;
KW fixation; resorption; osteoporosis; osteoporosis; hypoparathyroidism.
XX Synthetic.
XX
XX Key Location/Qualifiers
PH Modified-site 36
FT /note= "in amide form"
FT
XX GB2269176-A.
XX
XX 02-FEB-1994.
XX
XX 12-JUL-1993; 93GB-00014384.
XX
XX 15-JUL-1992; 92GB-00015009.
XX 18-DEC-1992; 92GB-00026415.
XX 23-DEC-1992; 92GB-00026859.
XX 23-DEC-1992; 92GB-00026861.
XX 28-JAN-1993; 93GB-00001691.
XX 28-JAN-1993; 93GB-00001692.
XX 14-APR-1993; 93GB-00007673.
XX 19-APR-1993; 93GB-00008033.
XX (SANO ) SANDOZ LTD.
XX
XX Lewis I, Schneider H, Waelchli R, Rainer A;
PI WPI; 1994-018352/03.
XX
XX New active para-thyroid hormone variants - used for treating or
XX preventing osteoporosis etc.
XX
XX Example 269; Page 46; 92pp; English.
XX
XX This peptide is an example of a highly generic formula covering
XX parathyroid hormone variants useful for treating or preventing bone
XX conditions associated with calcium depletion/resorption, in cases where
XX calcium fixation is required (esp. osteoporosis) or to treat
XX hypoparathyroidism
XX
XX Sequence 36 AA;
XX
XX Query Match 80.6%; Score 129; DB 2; Length 36;
XX Best Local Similarity 83.9%; Pred.No. 3e-10;
XX Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 AVSEIQLMHGGGGGLNSMERVEWLRKQLQDV 31
XX :||||||| | |||||||||
XX 1 SVSEIQLMHNAGKHLNSMERVEWLRKQLQDV 31
XX
XX RESULT 7
XX AAY98015
XX ID AAY98015 standard; peptide; 33 AA.
XX
XX AC AAY98015;
XX
XX 04-SEP-2000 (first entry)
XX
XX Human amino-terminal modified parathyroid hormone analogue # 6.
XX
XX Parathyroid hormone peptide; PTH; renal cell; osseous cell; human;
XX signal transduction; osteoporosis; amino-terminal modification;
XX bone disease; parathyroid hormone receptor; osteopenia;
XX hypoparathyroidism; fracture repair; hypercalcaemia; cancer; osteopathic.
XX
XX Homo sapiens.
XX
```

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PH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Ala is desamino residue"
XX
XX WO200031137-A1.
XX
XX 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-US027656.
XX
XX 25-NOV-1998; 98US-0110152P.
XX
XX (BRIN/) BRINGHURST F R.
XX (TAKA/) TAKASU H.
XX (GARD/) GARDELLA T J.
XX
XX Bringhurst FR, Takasu H, Gardella TJ;
XX WPI; 2000-400045/34.
XX
XX New parathyroid hormone (PTH) analogs having one or more amino acid
XX substitutions that confer PTH-1/PTH-2 receptor agonist properties, useful
XX for treating old age osteoporosis and post-menopausal osteoporosis.
XX
XX Disclosure; Page 64; 69pp; English.
XX
XX Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
XX cells, initiating signal transduction. It has been identified that the
XX carboxyl terminal of PTH is important for PTH receptor binding, while the
XX amino terminal is important for signal transduction. The present sequence
XX is a human PTH peptide, with an amino-terminal modification which results
XX in effective activation of the PTH-2 receptor and therefore downstream
XX signalling. Aberrant PTH activity has been implicated in a number of
XX disorders: osteoporosis, osteopenia, hypoparathyroidism and
XX hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
XX and a variety of cancers: breast, lung and prostate carcinoma, multiple
XX myeloma and epidermoid cancers of the head, neck and oesophagus. This
XX peptide would be suitable for prophylaxis and treatment of the above
XX disorders. In addition, the present sequence would be suitable for
XX fracture repair. The present sequence is modified to have a desamino
XX residue at position 1
XX
XX Sequence 33 AA;
XX
XX Query Match 80.0%; Score 128; DB 3; Length 33;
XX Best Local Similarity 87.1%; Pred.No. 3.8e-10;
XX Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 AVSEIQLMHGGGGGLNSMERVEWLRKQLQDV 31
XX :||||||| | |||||||||
XX 1 AVSEIQLMHNAGKHLNSMERVEWLRKQLQDV 31
XX
XX RESULT 8
XX AAW17941
XX ID AAW17941 standard; peptide; 34 AA.
XX
XX AC AAW17941;
XX
XX 29-JUL-1997 (first entry)
XX
XX Human parathyroid hormone analogue [Chall]hPTH(1-34)NH2.
XX
XX Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
XX bone fracture.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "Cyclohexylalanine (Cha)"
FT
```

```

PF 08-DEC-1997; 97WO-US022498.
XX
XX 07-JAN-1997; 97US-00779768.
XX 07-MAR-1997; 97US-00813534.
XX
XX (BIOM-) BIOMEASURE INC.
XX
XX PA
XX
XX Dong ZX;
XX
XX MPI; 1998-399065/34.
XX
XX Parathyroid hormone analogue peptide compounds - used for stimulating
XX bone growth, e.g. in treatment of bone fractures or osteoporosis.
XX
XX Claim 6; Page; 24pp; English.
XX
XX The invention relates to peptides of formula (I) containing at least one
XX Acc (i.e. 1-amino-1-(3-9C cycloalkane)-carboxylic acid) residue.
XX CC (R1) A1-Val-A3-Glu-A5-Gln-A7-A8-His-Asn-A11-A12-Lys-His-A15-A-16-A17-
XX CC A-18-A19-Arg-A21-A22-A23-A24-Arg-Lys-A27-A28-A29-A30-A31-A32-A33-A34-R3
XX CC (1); where A1 = Ser, Ala or Dap; A3, A17 = Ser, Thr or Alb; A5, A7, A11,
XX CC A15 = Leu, Nle, Ile, Cha, beta-Nal, Trp, Pal, Acc, Phe or p-(X)-Phe; X =
XX CC OH, halo or Me; A8 = Met, Nva, Leu, Val, Ile, Cha, Acc or Nle; A12 = Gly,
XX CC OH, halo or Me; A16 = Ser, Asn, Ala, Leu, Val, Ile, Cha, Acc or Met; A22 =
XX CC Nle, Acc, Cha or Alb; A19 = Glu or Alb; A21 = Val, Acc, Cha or Met; A22 =
XX CC Acc or Glu; A'23 = Trp, Acc or Cha; A24, A28 = Leu, Acc or Cha; A27 =
XX CC Lys, Alb, Leu, hArg, Gln, Acc or Cha; A29 = Glu, Acc or Alb; A30 = Asp or
XX CC Lys; A31 = Val, Leu, Nle, Acc or Cha, or is deleted; A32 = His or is
XX CC deleted; A33 = Asn or is deleted; A34 = Phe, Tyr, Amp or Alb, or is
XX CC deleted; R1, R2 = H, 1-12C alkyl, 2-12C alkenyl, 7-20C phenylalkyl, 11-20C
XX CC naphthylalkyl, 1-12C hydroxyalkyl, 2-12C hydroxyalkenyl, 7-20C
XX CC hydroxyphenylalkyl or 11-20C hydroxy-naphthylalkyl; one of R1 and R2 may
XX CC also = COE; E = 1-12C alkyl, 2-12C alkenyl, 7-20C phenylalkyl, 11-20C
XX CC naphthylalkyl, 1-12C hydroxyalkyl, 2-12C hydroxyalkenyl, 7-20C
XX CC hydroxyphenylalkyl or 11-20C hydroxy-naphthylalkyl; R3 = OH, NH2, 1-12C
XX CC alkoxy or -NH-Y-CH2-Z; Y = 1-12C hydrocarbyl; Z = H, OH, COOH or CONH2.
XX CC The peptides are variants of fragments of parathyroid hormone (PTH) or
XX CC parathyroid hormone-related protein (PTHrP). They stimulate bone growth,
XX CC and are useful in the treatment of diseases or disorders associated with
XX CC bone growth deficiency, e.g. osteoporosis and bone fractures. They are
XX CC optionally used in conjunction with anti-resorptive therapy, e.g. with
XX CC bis-phosphonates or calcitonin. The present sequence represents a
XX CC specifically claimed peptide. NB: This sequence is not shown explicitly
XX CC in the patent but was generated using the sequence of human parathyroid
XX CC hormone as shown in Entrez Locus Number AAA29146
XX
XX SQ Sequence 34 AA;
XX
XX Query Match 80.0%; Score 128; DB 2; Length 34;
XX Best Local Similarity 83.9%; Pred. No. 3.9e-10;
XX Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0
XX
XX QY 1 AVSEIQLMHGGGGGLNSMERVEWLRLKKLQDV 31
XX :||||| ||||| ||||| ||||| |||||
XX Db 1 SVSEIQLMHXXKHLSNMRVEWLRLKKLQDV 31
XX
XX RESULT 10
XX AAY98014
XX ID AAY98014 standard; peptide; 34 AA.
XX
XX XX
XX AC AAY98014;
XX
XX XX
XX 04-SEP-2000 (first entry)
XX
XX Human amino-terminal modified parathyroid hormone analogue # 5.
XX
XX Parathyroid hormone peptide; PTH; renal cell; osseous cell; human;
XX signal transduction; osteoporosis; amino-terminal modification;
XX bone disease; parathyroid hormone receptor; osteopaenia;
XX hypoparathyroidism; fracture repair; hypercalcaemia; cancer; osteopathic.
XX
XX OS Homo sapiens.

```

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XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX PN /note= "Ala is desamino residue"
XX XX WO200031137-A1.
XX XX 02-JUN-2000.
XX XX 23-NOV-1999; 99WO-US027656.
XX XX 25-NOV-1998; 98US-0110152P.
XX XX (BRIN/) BRINGHURST F R.
XX XX (TAKA/) TAKASU H.
XX XX (GARD/) GARDELLA T J.
XX XX Bringhamst FR, Takasu H, Gardella TJ;
XX XX WPI; 2000-400045/34.
XX DR New parathyroid hormone (PTH) analogs having one or more amino acid
XX FT substitutions that confer PTH-1/PTH-2 receptor agonist properties, useful
XX FT for treating old age osteoporosis and post-menopausal osteoporosis.
XX XX Claim 3; Page 63; 69pp; English.
XX XX Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
XX CC cells, initiating signal transduction. It has been identified that the
XX CC carboxyl terminal of PTH is important for PTH receptor binding, while the
XX CC amino terminal is important for signal transduction. The present sequence
XX CC is a human PTH peptide, with an amino-terminal modification which results
XX CC in effective activation of the PTH-2 receptor and therefore downstream
XX CC signalling. Aberrant PTH activity has been implicated in a number of
XX CC disorders: osteoporosis, osteopenia, hypoparathyroidism and
XX CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephrona
XX CC and a variety of cancers: breast, lung and prostate carcinoma, multiple
XX CC myeloma and epidermoid cancers of the head, neck and oesophagus. This
XX CC peptide would be suitable for prophylaxis and treatment of the above
XX CC disorders. In addition, the present sequence would be suitable for
XX CC fracture repair. The present sequence is modified to have a desamino
XX CC residue at position 1
XX XX Sequence 34 AA;
XX SQ Query Match 80.0%; Score 128; DB 3; Length 34;
XX Best Local Similarity 87.1%; Pred. No. 3.9e-10;
XX Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX QY 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
XX Db ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
XX RESULT 11
XX AAR58248
XX ID AAR58248 standard; peptide; 36 AA.
XX AC AAR58248;
XX XX 20-SEP-1994 (first entry)
XX DT N-Dimethyl-L-[Ala1]-hPTH(1-36)-NH2.
XX DE Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;
XX KW fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
XX XX Synthetic.
XX OS Key Location/Qualifiers
XX PH Modified-site 1
XX FT /label= Other
XX FT /note= "N-Dimethyl-Ala."
XX FT
```

```
FT Modified-site 36
XX /note= "in amide form"
XX PN GB2269176-A.
XX XX 02-FEB-1994.
XX PD 12-JUL-1993; 93GB-00014384.
XX PF 15-JUL-1992; 92GB-00015009.
XX PR 18-DEC-1992; 92GB-00026415.
XX PR 23-DEC-1992; 92GB-00026859.
XX PR 23-DEC-1992; 92GB-00026861.
XX PR 28-JAN-1993; 93GB-00001691.
XX PR 28-JAN-1993; 93GB-00001692.
XX PR 14-APR-1993; 93GB-00007673.
XX PR 19-APR-1993; 93GB-00008033.
XX XX (SANO ) SANDOZ LTD.
XX XX Lewis I, Schneider H, Waelchli R, Rainer A;
XX XX WPI; 1994-018352/03.
XX DR New active para-thyroid hormone variants - used for treating or
XX FT preventing osteoporosis etc.
XX PT Example 244; Page 45; 92pp; English.
XX XX This peptide is an example of a highly generic formula covering
XX CC parathyroid hormone variants useful for treating or preventing bone
XX CC conditions associated with calcium depletion/resorption, in cases where
XX CC calcium fixation is required (esp. osteoporosis) or to treat
XX CC hypoparathyroidism
XX XX Sequence 36 AA;
XX SQ Query Match 80.0%; Score 128; DB 2; Length 36;
XX Best Local Similarity 87.1%; Pred. No. 4.1e-10;
XX Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX QY 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
XX Db ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
XX RESULT 12
XX AAR58026
XX ID AAR58026 standard; peptide; 36 AA.
XX AC AAR58026;
XX XX 20-SEP-1994 (first entry)
XX DT N-alpha-methyl[Ala1] parathyroid hormone(1-36) .
XX DE Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;
XX KW fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
XX XX Synthetic.
XX OS Key Location/Qualifiers
XX PH Modified-site 1
XX FT /note= "N-alpha-methyl-Ala replaces wild-type Ser residue
XX FT at position 1"
XX FT GB2269176-A.
XX PN 02-FEB-1994.
XX PD 12-JUL-1993; 93GB-00014384.
XX PF 15-JUL-1992; 92GB-00015009.
XX PR
```

PR 18-DEC-1992; 92GB-00026415.  
PR 23-DEC-1992; 92GB-00026859.  
PR 23-DEC-1992; 92GB-00026861.  
PR 28-JAN-1993; 93GB-00001691.  
PR 28-JAN-1993; 93GB-00001692.  
PR 14-APR-1993; 93GB-00007673.  
PR 19-APR-1993; 93GB-00008033.  
XX (SANO ) SANDOZ LTD.  
XX Lewis I, Schneider H, Waelchli R, Rainer A;  
PI WPI; 1994-018352/03.  
XX New active para-thyroid hormone variants - used for treating or  
PT preventing osteoporosis etc.  
XX Example 12; Page 35; 92pp; English.  
XX This peptide is an example of a highly generic formula covering  
CC parathyroid hormone variants useful for treating or preventing bone  
CC conditions associated with calcium depletion/resorption, in cases where  
CC calcium fixation is required (esp. osteoporosis) or to treat  
CC hypoparathyroidism  
XX Sequence 36 AA;  
SQ Query Match 80.0%; Score 128; DB 2; Length 36;  
Best Local Similarity 87.1%; Pred. No. 4.1e-10;  
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 AVSEIQLMHGGGGGLNSMERVEWLKRLQDV 31  
DB 1 AVSEIQLMHNLGKHLNSMERVEWLKRLQDV 31  
RESULT 13  
AAR58262  
ID AAR58262 standard; peptide; 36 AA.  
XX AAR58262;  
AC  
XX 20-SEP-1994 (first entry)  
DT [Ala1]-hPTH(1-36)-NH2.  
DE Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;  
KW fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.  
XX Synthetic.  
XX Key Location/Qualifiers  
FH Modified-site 36 /note= "in amide form"  
FT  
FT  
XX GB2269176-A.  
XX 02-FEB-1994.  
XX 12-JUL-1993; 93GB-00014384.  
XX 15-JUL-1992; 92GB-00015009.  
PR 18-DEC-1992; 92GB-00026415.  
PR 23-DEC-1992; 92GB-00026859.  
PR 23-DEC-1992; 92GB-00026861.  
PR 28-JAN-1993; 93GB-00001691.  
PR 28-JAN-1993; 93GB-00001692.  
PR 14-APR-1993; 93GB-00007673.  
PR 19-APR-1993; 93GB-00008033.  
XX (SANO ) SANDOZ LTD.  
XX Lewis I, Schneider H, Waelchli R, Rainer A;  
PI

XX WPI; 1994-018352/03.  
DR New active para-thyroid hormone variants - used for treating or  
XX preventing osteoporosis etc.  
PT Example 260; Page 46; 92pp; English.  
XX This peptide is an example of a highly generic formula covering  
CC parathyroid hormone variants useful for treating or preventing bone  
CC conditions associated with calcium depletion/resorption, in cases where  
CC calcium fixation is required (esp. osteoporosis) or to treat  
CC hypoparathyroidism  
XX Sequence 36 AA;  
SQ Query Match 80.0%; Score 128; DB 2; Length 36;  
Best Local Similarity 87.1%; Pred. No. 4.1e-10;  
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 AVSEIQLMHGGGGGLNSMERVEWLKRLQDV 31  
DB 1 AVSEIQLMHNLGKHLNSMERVEWLKRLQDV 31  
RESULT 14  
AAR58019  
ID AAR58019 standard; peptide; 38 AA.  
XX AAR58019;  
AC  
XX 20-SEP-1994 (first entry)  
DT N-alpha-methyl[Ala1] parathyroid hormone(1-38).  
DE Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;  
KW fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.  
XX Synthetic.  
XX Key Location/Qualifiers  
FH Modified-site 1 /note= "N-alpha-methyl-Ala replaces wild-type Ser residue  
FT at position 1"  
FT  
XX GB2269176-A.  
XX 02-FEB-1994.  
XX 12-JUL-1993; 93GB-00014384.  
XX 15-JUL-1992; 92GB-00015009.  
PR 18-DEC-1992; 92GB-00026415.  
PR 23-DEC-1992; 92GB-00026859.  
PR 23-DEC-1992; 92GB-00026861.  
PR 28-JAN-1993; 93GB-00001691.  
PR 28-JAN-1993; 93GB-00001692.  
PR 14-APR-1993; 93GB-00007673.  
PR 19-APR-1993; 93GB-00008033.  
XX (SANO ) SANDOZ LTD.  
XX Lewis I, Schneider H, Waelchli R, Rainer A;  
PI WPI; 1994-018352/03.  
XX New active para-thyroid hormone variants - used for treating or  
PT preventing osteoporosis etc.  
XX Example 4; Page 34; 92pp; English.  
XX This peptide is an example of a highly generic formula covering  
CC parathyroid hormone variants useful for treating or preventing bone

CC conditions associated with calcium depletion/resorption, in cases where  
CC calcium fixation is required (esp. osteoporosis) or to treat  
CC hypoparathyroidism  
XX  
SQ Sequence 38 AA;  
Query Match 80.0%; Score 128; DB 2; Length 38;  
Best Local Similarity 87.1%; Pred. No. 4.4e-10; Indels 0; Gaps 0;  
Matches 27; Conservative 4; Mismatches 4;  
Oy 1 AVSEIQLMHGGGGGLNSMERVWLKRLQDV 31  
Db 1 AVSEIQLMHGGGGGLNSMERVWLKRLQDV 31  
RESULT 15  
AA96974  
ID AAY96974 standard; peptide; 31 AA.  
XX  
AC AAY96974;  
XX  
DT 31-OCT-2000 (first entry)  
XX  
DE Parathyroid hormone functional domain conjugate peptide PG9.  
XX  
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;  
KW resorption; remodeling; tether1; osteoporosis.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..5  
FT /label= PTH N-terminal\_signaling\_domain  
FT /note= "residues 1-5"  
FT Peptide 6..14  
FT /label= linker  
FT Peptide 15..31  
FT /label= PTH C-terminal\_binding\_portion  
FT /note= "residues 15-31"  
XX  
FN WC200039278-A2.  
XX  
PD 06-JUL-2000.  
XX  
PF 30-DEC-1999; 99WO-US031108.  
XX  
PR 31-DEC-1998; 98US-0114577P.  
XX  
XX (GARD/) GARDELLA T J.  
PA (KRON/) KRONENBERG H M.  
PA (POTT/) POTTS J T.  
PA (JUEP/) JUEPPNER H.  
XX  
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
PI WPI; 2000-452384/39.  
XX  
DR N-PSDB; AAA51731.  
XX  
XX New compound comprising an amino terminal signaling functional domain  
PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
PT treating mammalian conditions characterized by decreases in bone mass.  
PT  
PS Claim 7; Page 93; 119pp; English.  
XX  
XX Compounds of the structure or formula S-(L) n-B, R1-S-(L) n-R or S-(L) n  
CC -R are new S is an amino terminal signaling functional domain of  
CC parathyroid hormone (PTH). L is a linker molecule present n times (where  
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34). R1 is the  
CC PTH-1 receptor signal sequence; and R is a portion of PTH-1 receptor  
CC sequence. The new compounds are used for treating mammalian conditions  
CC characterized by decreases in bone mass, determining rates of bone

CC reformation, bone resorption and/or bone remodeling, treating diseases  
CC and disorders associated with decreased tether1 activity, increasing CAMP  
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
CC non-peptide PTH (claimed). The new compound can be administered by  
CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
CC regular injections to treat osteoporosis  
XX  
SQ Sequence 31 AA;  
Query Match 79.4%; Score 127; DB 3; Length 31;  
Best Local Similarity 87.1%; Pred. No. 4.8e-10;  
Matches 27; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
Oy 1 AVSEIQLMHGGGGGLNSMERVWLKRLQDV 31  
Db 1 AVSEIQMGGGGGGLNSMERVWLKRLQDV 31  
Search completed: November 21, 2005, 16:10:11  
Job time : 142.5 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 16:05:13 ; Search time 23.5 Seconds  
(without alignments)  
126.924 Million cell updates/sec

Title: US-09-475-158A-3  
Perfect score: 160  
Sequence: 1 AVSIIQLMHGGGGLNSMERVELRKKLQDV 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80: \*  
1: Pirl: \*  
2: Pirl2: \*  
3: Pirl3: \*  
4: Pirl4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	125	78.1	115	1 PTHU	parathyroid hormon
2	119	74.4	115	1 PTHO	parathyroid hormon
3	117	73.1	115	1 PTPG	parathyroid hormon
4	116	72.5	115	2 JC4202	parathyroid hormon
5	110	68.8	115	2 A05091	parathyroid hormon
6	105	65.6	105	2 I51851	parathyroid hormon
7	85	53.1	119	2 A34937	parathyroid hormon
8	62	38.8	641	2 B43777	choline O-acetyltr
9	62	38.8	644	2 A48319	choline O-acetyltr
10	60	37.5	626	2 A55720	carnitine O-acetyl
11	59	36.9	990	2 T03784	probable receptor
12	57	35.6	110	2 D69651	PTS lichenan-speci
13	56	35.0	399	1 HMXRH2	sigma 1 protein -
14	56	35.0	462	2 C34829	sigma 1 protein -
15	56	35.0	627	2 S52782	carnitine acetyltr
16	56	35.0	641	2 A39961	choline O-acetyltr
17	56	35.0	748	2 A60202	choline O-acetyltr
18	55	34.4	463	1 S74845	tLdD homolog slr08
19	55	34.4	614	2 T18745	hypothetical prote
20	54	33.8	627	2 S53369	carnitine O-acetyl
21	53	33.1	534	2 S62572	hypothetical prote
22	52	32.5	225	2 S67772	hypothetical prote
23	52	32.5	786	2 A53939	kinasin homolog KH
24	51.5	32.2	421	2 T10190	L-ascorbate peroxi
25	51	31.9	258	2 I39767	acetylglutamate ki
26	51	31.9	588	2 T45539	moad protein limpo
27	50.5	31.6	319	2 T45980	hypothetical prote
28	50.5	31.6	1375	2 F82336	DNA-directed RNA p
29	50	31.2	443	1 BVBVRI	mevalonate kinase

## ALIGNMENTS

### RESULT 1

PTHU

parathyroid hormone precursor [validated] - human

N:Alternate names: proparathyroid hormone

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence revision 19-Jan-1996 #text change 09-Jul-2004

C:Accession: A19339; S53790; A93169; A93789; A93783; A90426; A94410; I38

R:Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J

Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983

A:Title: Nucleotide sequence of the human parathyroid hormone gene.

A:Reference number: A19339; MUID:83169834; PMID:6220408

A:Accession: A19339

A:Molecule type: DNA

A:Residues: 1-115 <VAS>

A:Cross-references: UNIPROT:P01270; UNIPARC:UPI000013290A; GB:J00301; NID:gl90702; PIDN:

R:Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.

Biol. Chem. Hoppe-Seyler 375, 821-824, 1994

A:Title: Purification of meprin from human kidney and its role in parathyroid hormone de

A:Reference number: S53790; MUID:95225988; PMID:7710697

A:Accession: S53790

A:Molecule type: protein

A:Residues: 'X',33,'X',35-46;65-84;105-110 <YAM>

A:Cross-references: UNIPARC:UPI00001734E1; UNIPARC:UPI00001734E2; UNIPARC:UPI00001734E3

A:Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also occurre

R:Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.

Nature 249, 155-157, 1974

A:Title: Structural analysis of human parathyroid hormone by a new microsequencing at

A:Reference number: A93169; MUID:74174967; PMID:4833516

A:Accession: A93169

A:Molecule type: protein

A:Residues: 26-37 <JAC>

A:Cross-references: UNIPARC:UPI00001734E4

R:Olstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik, V.

Eur. J. Biochem. 205, 311-319, 1992

A:Title: Isolation and characterization of two biologically active O-glycosylated forms

action.

A:Reference number: S21199; MUID:92209518; PMID:1555591

A:Accession: S21199

A:Molecule type: protein

A:Residues: 32-114,'N' <OLS>

A:Cross-references: UNIPARC:UPI00001734E5

A:Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylation,

R:Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L.H

Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974

A:Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyroid

A:Reference number: A93789; MUID:74111656; PMID:4521809

A:Accession: A93789

A:Molecule type: protein

A:Residues: 32-68 <NIA>

A:Cross-references: UNIPARC:UPI000002DA05

R:Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D.

Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

retinoblastoma bin  
hypothetical prote  
hypothetical prote  
pur operon repress  
activator of purin  
acetyl xylan ester  
probable DNA bindi  
choline O-acetyltr  
hypothetical prote  
hypothetical prote  
virulence-associat  
parathyroid hormon  
hypothetical prote  
Mgpa operon hypoth  
amidase [EC 3.5.1.

A:Molecule type: mRNA  
A:Residues: 1-115 <WE2>  
A:CROSS-references: UNIPARC:UPI0000132907; GB:J00024; NID:G153642; PID:5  
R:Weaver, C.A.; Gordon, D.F.

Mol. Cell. Endocrinol. 28, 411-424, 1982  
A:Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.  
A:Reference number: 145976; MUID:83105964; PMID:6185374

A:Accession: 145976

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-115 <WE3>

A:Cross-references: UNIPARC:UPI0000132907; GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:

C:Genetics:

A:Gene: PTH

A:Introns: 29/2

C:Superfamily: parathyroid hormone; parathyroid hormone homology

C:Keywords: hormone

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-115/Product: parathyroid hormone #status experimental <PMAT>

F:26-31/Domain: propeptide #status experimental <PRO>

F:30-64/Domain: parathyroid hormone homology <PTH>

F:32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 74.4%; Score 119; DB 1; Length 115;

Best Local Similarity 80.6%; Pred. No. 1.2e-08; Mismatches 5; Indels 0; Gaps 0;

Matches 25; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Matches 25; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Matches 25; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Matches 25; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Matches 25; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Matches 25; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Matches 25; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Matches 25; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Matches 25; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

R.Ishii, K.; Oda, Y.; Ichikawa, T.; Deguchi, T.  
Brain Res. Mol. Brain Res. 7, 151-159, 1990  
A>Title: Complementary DNAs for choline acetyltransferase from spinal cords of rat and m  
A.Reference number: A43777; MUID:90251122; PMID:2160042  
A.Accession: B43777  
A>Status: preliminary; not compared with conceptual translation  
A.Molecule type: mRNA  
A.Residues: 1-641 <ISH>  
A.Cross-references: UNIPROT:Q03059; UNIPARC:UPI0000017535E  
R.Misawa, H.; Ishii, K.; Deguchi, T.  
J. Biol. Chem. 267, 20392-20399, 1992  
A>Title: Gene expression of mouse choline acetyltransferase. Alternative splicing and ide  
A.Reference number: A44023; MUID:93015919; PMID:1400357  
A.Accession: A44023  
A>Status: preliminary; not compared with conceptual translation  
A.Molecule type: DNA; mRNA  
A.Residues: 1-219 <MS>  
A.Cross-references: UNIPARC:UPI000016CC80; GB:D12487; NID:G220366; PIDN:BAA02056.1; PID:G  
A.Note: sequence extracted from NCBI backbone (NCBIP:115801)  
C:Superfamily: carnitine O-acetyltransferase  
C:Keywords: acyltransferase; coenzyme A

Query Match 38.8%; Score 62; DB 2; Length 641;  
Best Local Similarity 51.9%; Pred. No. 2.3;  
Matches 14; Conservative 2; Mismatches 9; Indels 2; Gaps 1;

QY 5 IQLMHGGGGGLNSMERVWLRLKQLQDV 31  
DB 298 LQLLHGGGCSLNGNR--WYDKSLQFV 322

RESULT 9  
A48319  
Choline O-acetyltransferase (EC 2.3.1.6) - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
A.Accession: A48319; A43777; A4981; A56876  
R.Brice, A.; Bertrand, S.; Raynaud, B.; Anstieau, S.; Coppola, T.; Weber, M.J.; Mallet, J. J.  
J. Neurosci. Res. 23, 266-273, 1989  
A>Title: Complete sequence of a cDNA encoding an active rat choline acetyltransferase: a  
A.Reference number: A48319; MUID:89362560; PMID:2570161  
A.Accession: A48319  
A>Status: preliminary; not compared with conceptual translation  
A.Molecule type: mRNA  
A.Residues: 1-644 <BR1>  
A.Cross-references: UNIPROT:P32738; UNIPARC:UPI000017535A  
R.Ishii, K.; Oda, Y.; Ichikawa, T.; Deguchi, T.  
Brain Res. Mol. Brain Res. 7, 151-159, 1990  
A>Title: Complementary DNAs for choline acetyltransferase from spinal cords of rat and m  
A.Reference number: A43777; MUID:90251122; PMID:2160042  
A.Accession: A43777  
A>Status: preliminary; not compared with conceptual translation  
A.Molecule type: mRNA  
A.Residues: 1-233 'N' 235-376, 'L', 378-498, 'HKQ', 502-569, 'N', 571-634, 'SQAKQS' <ISH>  
A.Cross-references: UNIPARC:UPI000017535B  
R.Mori, N.; Tajima, Y.; Sakaguchi, H.; Vandenbergh, D.J.; Nawa, H.; Salvaterra, P.M.  
Brain Res. Mol. Brain Res. 17, 101-111, 1993  
A>Title: Partial cloning of the rat choline acetyltransferase gene and in situ localizat  
A.Reference number: A4981; MUID:93164851; PMID:8381893  
A.Accession: A4981  
A>Status: preliminary  
A.Molecule type: nucleic acid  
A.Residues: 397-437 <MOR>  
A.Cross-references: UNIPARC:UPI000017535C  
A>Note: sequence extracted from NCBI backbone (NCBIN:124964, NCBIP:124965)  
R.Kengaku, M.; Misawa, H.; Deguchi, T.  
Brain Res. Mol. Brain Res. 18, 71-76, 1993  
A>Title: Multiple mRNA species of choline acetyltransferase from rat spinal cord.  
A.Reference number: A56876; MUID:93240983; PMID:8479291  
A.Accession: A56876  
A>Status: preliminary  
A.Molecule type: mRNA  
A.Residues: 1-33 <KEN>

T03784  
probable receptor protein kinase - rice  
C:Species: Oryza sativa (rice)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 31-Dec-2004  
C:Accession: T03784  
R:Yu, Y.; Zhu, Q.; Lamb, C.  
Submitted to the EMBL Data Library, June 1995  
A:Description: Molecular cloning and characterization of a rice gene encoding leucine-rich  
A:Reference number: Z15083  
A:Accession: T03784  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-990 <XUY>  
A:Cross-references: UNIPROT:Q40699; UNIPARC:UPI00000A9030; EMBL:X89226; NID:gl263159; PFI  
A:Experimental source: cv. IR36, leaf  
C:Genetics:  
A:Gene: lrk2  
A:Introns: 870/1  
C:Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat ho

Query Match 36.9%; Score 59; DB 2; Length 990;  
Best Local Similarity 52.4%; Pred. No. 8.9;  
Matches 11; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 8 MHGGGGGLNSMERVENLKKKL 28  
| ||||| :|: ||:  
DB 625 MRGGGGGGLRLRWDSKKM 645

RESULT 12  
D69651  
PTS lichenan-specific enzyme IIA component lica - Bacillus subtilis  
N:Alternate names: probable cellobiose phosphotransferase enzyme III  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 31-Dec-2004  
C:Accession: D69651; S57761  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
C.; Bron, S.; Broutillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho  
C.; Ehrlich, S.D.; Emmertson, P.T.; Entian, K.D.; Errington, J.; Fabre, J.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Toasato, V.; Uchiyama  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: D69651  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-110 <KUN>  
A:Cross-references: UNIPROT:P46319; UNIPARC:UPI0000060C4F; GB:Z99123; GB:AL009126; NID:G  
A:Experimental source: strain 168  
R:Glaser, P.; Lubochinsky, B.; Danchin, A.  
Submitted to the EMBL Data Library, July 1995  
A:Description: Bacillus subtilis cel operon.  
A:Reference number: S57758  
A:Accession: S57761  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-110 <GLA>  
A:Cross-references: UNIPARC:UPI0000060C4F; EMBL:Z49992; NID:G895746; PIDN:CAA90287.1; PFI  
C:Genetics:  
A:Gene: lica  
A:Start codon: GTG  
C:Superfamily: phosphotransferase system, lactose/cellobiose-specific component IIA

Query Match 35.6%; Score 57; DB 2; Length 110;

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C.Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C.Accession: S52782
R.Brunner, S.; Kramar, K.; Hofbauer, R.
  submitted to the EMBL Data Library, March 1995
A.Description: A novel cell cycle regulated carnitine acetyltransferase in S3T3 cells.
A.Reference number: S52782
C.Accession: S52782
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-627 <BR>
A.Cross-references: UNIPROT:P47934; UNIPARC:UPI000002783E; EMBL:X85983; NID:G758631; PID:N
C.Superfamily: carnitine O-acetyltransferase

Query Match          35.0%; Score 56; DB 2; Length 627;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 12; Conservative 2; Mismatches 8; Indels 2; Gaps 1;

QY      6 QLMHGGGGGLNSMSEVWLKKLQ 29
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DB     308 QMLHGGGSKFNSGNR--WFDKTLQ 329

Search completed: November 21, 2005, 16:17:15
Job time : 24.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 15:55:27 ; Search time 146.5 Seconds  
(without alignments)  
149.293 Million cell updates/sec

Title: US-09-475-158A-3

Perfect score: 160

Sequence: 1 AVSEIQLMHGGGGLNSMERVEWLKQLQDV 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05\_80:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	78.1	115	1	PTHY_HUMAN
2	125	78.1	115	1	PTHY_MACFA
3	125	78.1	115	2	Q4VB48 HUMAN
4	121	75.6	86	2	Q9N1V0 equus caball
5	119	74.4	115	1	PTHY_BOVIN
6	117	73.1	115	1	PTHY_PIG
7	116	72.5	115	1	PTHY_CANFA
8	110	68.8	105	2	Q80WZ2_RAT
9	110	68.8	115	1	PTHY_RAT
10	109	68.1	115	1	PTHY_FELCA
11	108	67.5	115	2	Q9Z0L6 MOUSE
12	85	53.1	119	1	PTHY_CHICK
13	68	42.5	91	2	Q6W9J4_FUGRU
14	65	40.6	15	1	CB30_HYDMC
15	65	40.6	163	2	Q918E9_FUGRU
16	63	39.4	166	2	Q6H9R6_PLAFE
17	63	39.4	166	2	Q531Q0_PLAFE
18	62	38.8	99	2	Q6WQ24_BRARE
19	62	38.8	162	2	Q918U2_SPAAU
20	62	38.8	250	1	BT0H_AZOSE
21	62	38.8	625	1	Q8BQN4_MOUSE
22	62	38.8	639	1	CLAT_RAT
23	62	38.8	640	1	CLAT_MOUSE
24	62	38.8	645	2	Q8BQV2_MOUSE
25	60	37.5	102	2	Q5TLZ1_BRARE
26	60	37.5	107	2	Q6WQ25_BRARE
27	60	37.5	107	2	Q4TGY4_TETNG
28	60	37.5	530	2	Q4SRM4_TETNG
29	60	37.5	626	1	CACP_HUMAN
30	60	37.5	626	2	Q5T952_HUMAN
31	59	36.9	990	2	Q40699_ORYZA

32	58	36.2	177	2	Q4RSF3_TETNG	Q4rsf3 tetraodon n
33	57	35.6	31	2	Q91Y90_PERMA	Q91y90 peromyscus
34	57	35.6	31	2	Q91Y91_PERPL	Q91y91 peromyscus
35	57	35.6	110	1	PTJA_BAGSU	P46319 bacillus su
36	57	35.6	208	2	Q6FT33_CANGA	Q6ft33 candida gla
37	57	35.6	549	2	Q4J3M6_AZOVI	Q4j3m6 azotobacter
38	57	35.6	631	2	Q642H6_BRARE	Q642h6 brachydanio
39	57	35.6	994	2	Q5Z9N5_ORYSA	Q5z9n5 oryza sativ
40	57	35.6	994	2	Q8SB35_ORYSA	Q8sb35 oryza sativ
41	57	35.6	1449	2	Q4RPV8_TETNG	Q4rpv8 tetraodon n
42	56.5	35.3	232	2	Q6H658_ORYSA	Q6h658 oryza sativ
43	56	35.0	198	2	Q5SPK3_BRARE	Q5spk3 brachydanio
44	56	35.0	198	2	Q4VVA3_BRARE	Q4vva3 brachydanio
45	56	35.0	293	2	Q9FJF5_ARATH	Q9fjf5 arabidopsia

## ALIGNMENTS

### RESULT 1

PTHY_HUMAN	PTHY_HUMAN	STANDARD;	PRT;	115 AA.
ID	PTHY_HUMAN	STANDARD;	PRT;	115 AA.
AC	P01270;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone) .			
GN	Name=PTH;			
OS	Homo sapiens (Human) .			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RP	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=82150870; PubMed=6950381;			
RA	Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;			
RT	"Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone."			
RL	Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).			
RP	PROTEIN SEQUENCE OF 26-37.			
RX	MEDLINE=74174967; PubMed=4833516;			
RA	Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;			
RT	"Structural analysis of human parathyroid hormone by a new microsequencing approach."			
RL	Nature 249:155-157(1974).			
RP	PROTEIN SEQUENCE OF 26-40.			
RX	PubMed=15340161; DOI=10.1110/ps.04682504;			
RA	Zhang Z., Henzel W.J.;			
RT	"Signal peptide prediction based on analysis of experimentally verified cleavage sites."			
RL	Protein Sci. 13:2819-2824(2004).			
RP	PROTEIN SEQUENCE OF 32-68.			
RX	MEDLINE=74111656; PubMed=4521809;			
RA	Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,			
RT	O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;			
RL	"The amino-acid sequence of the amino-terminal 37 residues of human parathyroid hormone."			
RP	Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).			
RP	[6]			
RX	PROTEIN SEQUENCE OF 61-83 AND 84-115.			
RA	MEDLINE=79082855; PubMed=728431;			
RA	Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,			

RA Potts J.T. Jr.;  
 RT "Complete amino acid sequence of human parathyroid hormone.";  
 RL Biochemistry 17:5723-5729(1978).  
 RN [7]  
 RP PROTEIN SEQUENCE OF 75-100.  
 RA Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,  
 RA O'Riordan J.L.H., Potts J.T. Jr.;  
 RL (In) Talmadge R.V., Owen M., Parsons J.A. (eds.);  
 RL Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation,  
 RL Amsterdam (1975).  
 RN [8]  
 RP SEQUENCE REVISION.  
 RA MEDLINE=75146516; PubMed=1125201;  
 RA Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;  
 RT "A reinvestigation of the amino-terminal sequence of human parathyroid  
 RT hormone.";  
 RL Biochemistry 14:1842-1847(1975).  
 RN [9]  
 RP SYNTHESIS OF 32-65.  
 RA Tregear G.W., van Rietschoten J., Green E., Niall H.D., Keutmann H.T.,  
 RA Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;  
 RT "Solid-phase synthesis of the biologically active N-terminal 1-34  
 RT peptide of human parathyroid hormone.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).  
 RN [10]  
 RP SYNTHESIS OF 32-65.  
 RA Andreata R.H., Hartmann A., Joehl A., Kamber B., Maier R.,  
 RA Riniker B., Rittel W., Sieber P.;  
 RT "Synthesis of sequence 1-34 of human parathyroid hormone.";  
 RL Helv. Chim. Acta 56:470-473(1973).  
 RN [11]  
 RP STRUCTURE BY NMR OF 32-65.  
 RA MEDLINE=91299746; PubMed=2069952;  
 RA Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;  
 RT "Investigation of the solution structure of the human parathyroid  
 RT hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry, and  
 RT molecular dynamics calculations.";  
 RL Biochemistry 30:6936-6942(1991).  
 RN [12]  
 RP STRUCTURE BY NMR OF 32-65.  
 RA MEDLINE=93345518; PubMed=8344299;  
 RA Barden J.A., Cuthbertson R.M.;  
 RT "Stabilized NMR structure of human parathyroid hormone (1-34).";  
 RL Eur. J. Biochem. 215:315-321(1993).  
 RN [13]  
 RP STRUCTURE BY NMR OF 32-68.  
 RA MEDLINE=95318084; PubMed=7797503; DOI=10.1074/jbc.270.25.15194;  
 RA Marx U.C., Austermann S., Bayer P., Adermann K., Eychart A.,  
 RA Sticht H., Walter S., Schmid F.-X., Jaenicke R., Försmann W.-G.,  
 RA Roesch P.;  
 RT "Structure of human parathyroid hormone 1-37 in solution.";  
 RL J. Biol. Chem. 270:15194-15202(1995).  
 RN [14]  
 RP STRUCTURE BY NMR OF 32-70.  
 RA MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;  
 RA Marx U.C., Adermann K., Bayer P., Försmann W.-G., Roesch P.;  
 RT "Solution structures of human parathyroid hormone fragments hPTH(1-34)  
 RT and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";  
 RL Biochem. Biophys. Res. Commun. 267:213-220(2000).  
 RN [15]  
 RP VARIANT FTH ARG-18.  
 RA MEDLINE=91009811; PubMed=2212001;  
 RA Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,  
 RA Kronenberg H.M.;  
 RT "Mutation of the signal peptide-encoding region of the  
 RT preproparathyroid hormone gene in familial isolated  
 RT hypoparathyroidism.";  
 RL J. Clin. Invest. 86:1084-1087(1990).  
 RN [16]  
 RP VARIANT FTH PRO-23.  
 RA PubMed=10523031;

RA Sunthornthepvarakul T., Churesigaew S., Ngongarmratana S.;  
 RT "A novel mutation of the signal peptide of the preproparathyroid  
 RT hormone gene associated with autosomal recessive familial isolated  
 RT hypoparathyroidism.";  
 RL J. Clin. Endocrinol. Metab. 84:3792-3796(1999).  
 RN [17]  
 RP FUNCTION: PTH elevates calcium level by dissolving the salts in  
 CC bone and preventing their renal excretion.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC DISEASE: Defects in PTH are a cause of familial isolated  
 CC hypoparathyroidism (FIH) [MIM:146200]. FIH exist both as autosomal  
 CC dominant and recessive forms of hypoparathyroidism.  
 CC -1- SIMILARITY: Belongs to the parathyroid hormone family.  
 CC  
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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL; J00301; AAA50215.1; -; Genomic DNA.  
 CC EMBL; V00597; CAA23843.1; -; mRNA.  
 CC EMBL; A29146; CAA01956.1; -; Unassigned DNA.  
 CC PTR; A19339; PTHU.  
 CC PDB; 1BMX; NMR; @=32-70.  
 CC PDB; 1ET1; X-ray; A/B=32-65.  
 CC PDB; 1ET2; Model; A=32-65.  
 CC PDB; 1FVY; NMR; A=32-62.  
 CC PDB; 1HPH; NMR; @=32-68.  
 CC PDB; 1HPY; NMR; @=32-65.  
 CC PDB; 1HTH; NMR; @=32-65.  
 CC PDB; 1ZWA; NMR; @=32-65.  
 CC PDB; 1ZWB; NMR; @=33-68.  
 CC PDB; 1ZWD; NMR; @=34-68.  
 CC PDB; 1ZWE; NMR; @=35-68.  
 CC PDB; 1ZWF; NMR; @=35-68.  
 CC PDB; 1ZWG; NMR; @=35-68.  
 CC  
 CC EMBL; ENSG00000152266; Homo sapiens.  
 CC HGNC; HGNC:9608; PTH.  
 CC MIM; 168450; -;  
 CC MIN; 146200; -;  
 CC GO; GO:0005576; C:extracellular region; NAS.  
 CC GO; GO:0005179; F:hormone activity; TAS.  
 CC GO; GO:0045453; P:bone resorption; NAS.  
 CC GO; GO:0006874; P:calcium ion homeostasis; NAS.  
 CC GO; GO:0046058; P:cAMP metabolism; TAS.  
 CC GO; GO:0007267; P:cell-cell signaling; TAS.  
 CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.  
 CC GO; GO:0008628; P:induction of apoptosis by hormones; TAS.  
 CC GO; GO:0001501; P:skeletal development; TAS.  
 CC InterPro; IPR003625; Pthyrohm\_sub.  
 CC InterPro; IPR001501; Pthyrohm\_sub.  
 CC PANTHER; PTHR10541; Pthyrohm\_sub; 1.  
 CC Pfam; PF01279; Parathyroid; 1.  
 CC PIRSF; PIRSF001832; PTH; 1.  
 CC ProDom; PD010687; Pthyrohm\_sub; 1.  
 CC SMART; SM00087; PTH; 1.  
 CC PROSITE; PS00335; PARATHYROID; 1.  
 CC 3D-structure; Direct protein sequencing; Disease mutation; Hormone;  
 CC SIGNAL. 1 25 Parathyroid hormone.  
 CC PROPEP 26 31 C->R (in FIH; dominant; leads to  
 CC CHAIN 32 115 /FTID=VAR\_006047 inefficient processing of the precursor).  
 CC VARIANT 18 18 S...P (in FIH; recessive; might lead to  
 CC VARIANT 23 23 /FTID=VAR\_018464 inefficient processing of the precursor).  
 CC N -> D (in Ref. 6).  
 CC  
 CC CONFLICT 107 107  
 CC HELIX 34 64  
 CC SEQUENCE 115 AA; 12861 MW; 849015736AE5597 CRC64;  
 SQ  
 Query Match 78.1%; Score 125; DB 1; Length 115;



Best Local Similarity 83.9%; Pred. No. 1.3e-08;  
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy	1	AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV	31
		:	
Dd	32	SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV	62

## RESULT 2

PTHY_MACFA	STANDARD;	PRT;	115 AA.
ID	PTHY_MACFA		
AC	Q9XT35;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	10-MAY-2005 (Rel. 47, Last annotation update)		
DE	Parathyroid hormone precursor (Parathyrin) (PTH)		
GN	Names:PTH;		
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey)		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
OC	Cercopithecoidea; Cercopithecidae; Cercopithecinae; Macaca.		
OX	NCBI TaxID:9541;		

RV  
[1]  
BP  
NUCLEOTIDE SEQUENCE.

RA Nucleotide sequence of parathyroid gene in five species of macaque  
 RT Malavilithond S., Takenaka O.;  
 RT "Nucleotide sequences of parathyroid gene in five species of macaque  
 of Thailand.";  
 RT J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).  
 CC -1- FUNCTION: PTH elevates calcium level by dissolving the salts in  
 CC bone and preventing their renal excretion.  
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -I- SUBCELLULAR LOCATION: secreted.

CC -I- SIMILARITY: Belongs to the parathyroid hormone family.

-----  
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 CC use as long as its content is in no way modified and this statement is not  
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EMBL: AF130257: AAD42777.1: -: Genomic DNA:

DR IPK00141; Parathyroid\_hrm.  
DR IPK00362; Parathyroid\_sub.  
DR PTHR10541; Pthyroid\_sub; 1.  
DR PF01279; Parathyroid; 1.  
DR PIRSF01832; PTH; 1.  
DR PIRSF010687; Pthyroid\_sub; 1.  
DR SMART; SMO0087; PTH; 1.  
DR PROSITE; PS00315; PARATHYROID; 1.

KW	Hormone; Signal.		
FT	SIGNAL	1	25 By similarity.
FT	PROPEP	26	31 By similarity.
FT	CHAIN	32	115 Parathyroid hormone.
SO	SEQUENCE	115 AA: 12890 MW: 8C3500EF24BE	

Query Match 78.1%; Score 125; DB 1; Length 115;  
Best Local Similarity 83.9%; Pred. No. 1.3e-08;  
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY	1	AVSEIQLMHGGGGGINSMERVEWLRKKLQDV	31
		:	
n6	12	SVSEIQLMHNTGKHINSMERVEWLRKKLQDV	62

### RESULT 3

Q4VB48	HUMAN		
ID	Q4VB48_HUMAN	PRELIMINARY;	PRT; 115 AA.
AC	Q4VB48;		
DT	13-SEP-2005	(TrEMBLrel. 31, Created)	
DT	13-SEP-2005	(TrEMBLrel. 31, Last sequence update)	
DT	13-SEP-2005	(TrEMBLrel. 31, Last annotation update)	
DE	Parathyroid hormone, preproprotein.		
GN	Name=PTH;		

50 20 20 20 x0

Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
Homo.  
NCBI TaxID=9606;

NUCLEOTIDE SEQUENCE.

TISSUE=PCR rescued clones;  
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; more than 15,000 full-length human  
"generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

## [2] NUCLEOTIDE SEQUENCE

RC	NUCLEOTIDE SEQUENCE..	
RC	TISSUE=PCR rescued clones;	
RG	NIH MGC Project;	
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC096143; AAH96143.1; -; mRNA.	
DR	EMBL; BC096144; AAH96144.1; -; mRNA.	
DR	EMBL; BC096145; AAH96145.1; -; mRNA.	
DR	EMBL; BC096142; AAH96142.1; -; mRNA.	
DR	InterPro; IPR001415; Parathyroid hrm.	
DR	InterPro; IPR003625; Pthythorm_sub.	
DR	Pfam; PF01279; Parathyroid; 1.	
DR	PIRSP; PIRSF001832; PTH; 1.	
DR	ProDom; PD010687; Pchythorm_sub; 1.	
DR	SMART; SM00087; PTH; 1.	
DR	PROSITE; PS00335; PARATHYROID; 1.	
DR	SEQUENCE 115 AA: 12861 MW: 849015736A6E5597 CRC64;	
SO	SEQUENCE	

Query Match	78.1%	Score 125;	DB 2;	Length 115;
Best Local Similarity	83.9%	Pred. No. 1.3e-08;		
Matches	26;	Conservative	1;	Mismatches 4;
			Indels	0;
			Gaps	0;

Qy	Qz	Qx
1	AVSEIQLMHGGGGLNSMERVEWLRKKLQDV	31
	:	
32	SVSEIOTMHNIGKHI NSMERVEWLRKKLQDV	62

#### RESULT 4

Q9N1V0_HORSE	Q9N1V0_HORSE PRELIMINARY;	PRT; 86 AA.
AC	Q9N1V0;	
DT	01-OCT-2000 (T-EMBLrel. 15, Created)	
DT	01-OCT-2000 (T-EMBLrel. 15, Last sequence update)	
DT	01-JUN-2003 (T-EMBLrel. 24, Last annotation update)	
DE	Parathyroid hormone (Fragment).	
GN	Name=PTH;	
OS	Equus caballus (Horse)..	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus	
OX	NCBI_TaxID=9796;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RA	MEDLINE=20082971; PubMed=10613847; DOI=10.1101/gr.9.12.1239;	
RA	Catapano A.R., Shive Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,	

```

RA Bowling A.T., Murray J.D.;
RT "A comparative gene map of the horse (Equus caballus).";
RL Genome Res. 9:1239-1249(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Shue Y.-L., Caetano A.R., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA Murray J.D., Bowling A.T.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF134233; AAF62347.1; -, Genomic_DNA.
DR HSP; P01270; IET1.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthythorm_sub.
DR PANTHER; PTHR10541; Pthythorm_sub; 1.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthythorm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1
FT SEQUENCE 86 AA; 9805 MW; 253184EA681A2022 CRC64;
QY Query Match 75.6%; Score 121; DB 2; Length 86;
Best Local Similarity 80.6%; Pred. NO. 3.2e-08;
Matches 25; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Db 1 AVSFIQLMHGGGGLNSMERVELRKKLDQV 31
3 SVSFIQLMHNKLHNSVERVELRKKLDQV 33

RESULT 5
PTH BOVIN STANDARD; PRT; 115 AA.
AC P01268.
DC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=PTH;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=80056617; PubMed=388425;
RX Kronenberg H.M., McDewitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
RA Potts J.T. Jr., Rich A.;
RT "Cloning and nucleotide sequence of DNA coding for bovine
RT preproparathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82037785; PubMed=6170060;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Introduction by molecular cloning of artifactual inverted sequences
RT at the 5' terminus of the sense strand of bovine parathyroid hormone
RT cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83105964; PubMed=6185374; DOI=10.1016/0303-7207(82)90136-8;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
RL Mol. Cell. Endocrinol. 28:411-424(1982).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84262483; PubMed=6086460; DOI=10.1016/0378-1119(84)90149-5;
RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
RT "Isolation and complete nucleotide sequence of the gene for bovine
RT parathyroid hormone.";
```

```

RL Gene 28:319-329(1984).
RN [5]
RP PROTEIN SEQUENCE OF 26-115.
RX MEDLINE=74142666; PubMed=4522780;
RA Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
RA Conn D.V.;
RT "The N-terminal amino-acid sequence of bovine preparathyroid
RT hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
RN [6]
RP PROTEIN SEQUENCE OF 32-115.
RX MEDLINE=71076162; PubMed=5531031;
RX Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
RA Aurbach G.D., Potts J.T. Jr.;
RT "The amino acid sequence of bovine parathyroid hormone I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
RN [7]
RP PROTEIN SEQUENCE OF 32-115.
RX MEDLINE=71063634; PubMed=5275384;
RA Brewer H.B. Jr., Ronan R.;
RT "Bovine parathyroid hormone: amino acid sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE=71091588; PubMed=4322265;
RA Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
RA Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
RT "Synthesis of a biologically active N-terminal tetrapeptide
RT of parathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
RN [9]
RP STRUCTURE BY NMR OF 32-68.
RX MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;
RX Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
RT "Solution structures of human parathyroid hormone fragments hPTH(1-34)
RT and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";
RL Biochem. Biophys. Res. Commun. 267:213-220(2000).
CC !- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC bone and preventing their renal excretion.
CC !- SUBCELLULAR LOCATION: Secreted.
CC !- SIMILARITY: Belongs to the parathyroid hormone family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; V00106; CAA23439.1; -, mRNA.
CC EMBL; J00024; AAA30747.1; -, mRNA.
CC EMBL; K01938; AAA30749.1; -, Genomic_DNA.
CC EMBL; M25082; AAA30748.1; -, mRNA.
CC PIR; A24949; PTBO.
CC PDB; 1ZWC; NMR; @=32-68.
CC InterPro; IPR001415; Parathyrd_hrm.
CC InterPro; IPR003625; Pthythorm_sub.
CC PANTHER; PTHR10541; Pthythorm_sub; 1.
CC Pfam; PF01279; Parathyroid; 1.
CC PROSITE; PS00087; PTH; 1.
CC PROSITE; PS00335; PARATHYROID; 1.
CC PROSITE; PS00335; PARATHYROID; 1.
KW 3D-structure; Direct protein sequencing; Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 Parathyroid hormone.
FT CONFLICT 106 106 V -> G (in Ref. 4).
FT HELIX 37 40
FT TURN 41 42
FT TURN 51 52
FT TURN 53 60
FT TURN 61 63
FT SEQUENCE 115 AA; 12980 MW; 2ED246B348880710 CRC64;
SQ
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RESULT 8  
Q80WZ2 RAT  
ID Q80WZ2 RAT PRELIMINARY;  
PRT: 105 AA.

AC Q80W22;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothalamic parathyroid hormone.  
 GN Name=PTH-(1-84);  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;  
 RA Nutley M.T., Parimi S.A., Harvey S.;  
 RT "Sequence analysis of hypothalamic parathyroid hormone messenger  
 ribonucleic acid.";  
 RL Endocrinology 136:5600-5607(1995).  
 DR EMBL; 580127; AF032220.1; -; mRNA.  
 DR HSSP; P01270; 12WB.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR InterPro; IPR001415; Parathyrd\_hrm.  
 DR PANTHER; PTHR10541; Pthythorm\_sub.  
 DR Pfam; PF01279; Parathyroid; 1.  
 DR PIRSF; PIRSF001832; PTH; 1.  
 DR ProDom; PD010687; Pthythorm\_sub; 1.  
 DR SMART; SM00087; PTH; 1.  
 DR PROSITE; PS00335; PARATHYROID; 1.  
 SQ SEQUENCE 105 AA; 11684 MW; 18EE71B3F1CF5F70 CRC64;  
 Query Match 68.8%; Score 110; DB 2; Length 105;  
 Best Local Similarity 74.2%; Pred.No.1.1e-06;  
 Matches 23; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 AVSEIQLMHGGGGGLNSMERVWRKQLQDV 31  
 DQ 22 AVSEIQLMHNLGKHLASVERMQLKQLQDV 52  
 RESULT 9  
 ID\_PTH\_RAT STANDARD; PRT; 115 AA.  
 AC P04089; Q63473;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-NOV-1986 (Rel. 03, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Parathyroid hormone precursor (Parathyrin) (PTH).  
 GN Name=PTH;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidae; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=84135846; PubMed=6321505;  
 RA Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;  
 RT "Gene encoding parathyroid hormone. Nucleotide sequence of the rat  
 gene and deduced amino acid sequence of rat preproparathyroid  
 hormone.";  
 RL J. Biol. Chem. 259:3320-3329(1984).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=87316938; PubMed=3628009;  
 RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;  
 RT "Nucleotide sequence of a full-length cDNA clone encoding  
 preproparathyroid hormone from pig and rat.";  
 RL Nucleic Acids Res. 15:6740-6740(1987).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE OF 10-115.

RC TISSUE=Parathyroid;  
 RA Schmelzer H.-J., Gross G., Mayer H.;  
 RT "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid  
 hormone.";  
 RL Adv. Gene Technol. 21:228-229(1984).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE OF 32-115.  
 RC STRAIN=Sprague-Dawley; TISSUE=Brain, Liver, and Parathyroid;  
 RX MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;  
 RA Nutley M.T., Parimi S.A., Harvey S.;  
 RT "Sequence analysis of hypothalamic parathyroid hormone messenger  
 ribonucleic acid.";  
 RL Endocrinology 136:5600-5607(1995).  
 CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in  
 bone and preventing their renal excretion.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Hypothalamus and parathyroid gland.  
 CC -!- SIMILARITY: Belongs to the parathyroid hormone family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC EMBL; K01268; AAA41979.1; -; Genomic\_DNA.  
 DR EMBL; X05721; CAA25192.1; -; mRNA.  
 DR EMBL; M54875; AAA57156.1; -; mRNA.  
 DR PIR; S80127; -; NOT\_ANNOTATED\_CDS; mRNA.  
 DR PIR; A05091; A05091.  
 DR HSSP; P01270; 12WB.  
 DR Ensembl; ENSRNOG00000014318; Rattus norvegicus.  
 DR RGD; 3440; Pth.  
 DR InterPro; IPR001415; Parathyrd\_hrm.  
 DR InterPro; IPR003626; PTH related.  
 DR InterPro; IPR003625; Pthythorm\_sub.  
 DR PANTHER; PTHR10541; Pthythorm\_sub; 1.  
 DR Pfam; PF01279; Parathyroid; 1.  
 DR PIRSF; PIRSF001832; PTH; 1.  
 DR ProDom; PD013225; PTH related; 1.  
 DR ProDom; PD010687; Pthythorm\_sub; 1.  
 DR SMART; SM00087; PTH; 1.  
 DR PROSITE; PS00335; PARATHYROID; 1.  
 KW Hormone; Signal.  
 FT SIGNAL 1 25  
 FT PROPEP 26 31  
 FT CHAIN 32 115 parathyroid hormone.  
 FT CONFLICT 18 18 C -> Y (in Ref. 3).  
 FT CONFLICT 23 23 A -> T (in Ref. 3).  
 FT CONFLICT 33 33 V -> I (in Ref. 3).  
 FT CONFLICT 62 62 V -> G (in Ref. 3).  
 SQ SEQUENCE 115 AA; 12722 MW; 7B434CFCAS28B230 CRC64;  
 Query Match 68.8%; Score 110; DB 1; Length 115;  
 Best Local Similarity 74.2%; Pred.No.1.3e-06;  
 Matches 23; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 AVSEIQLMHGGGGGLNSMERVWRKQLQDV 31  
 DQ 32 AVSEIQLMHNLGKHLASVERMQLKQLQDV 62  
 RESULT 10  
 ID\_PTH\_FELCA STANDARD; PRT; 115 AA.  
 AC Q9GL67;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Parathyroid hormone precursor (Parathyrin) (PTH).  
 GN Name=PTH;  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.G., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
"generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";   
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[3]  
NUCLEOTIDE SEQUENCE.  
TISSUE=Thyroid;  
NIH MGC Project;  
Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.  
EMBL; AF06075; AAC99656.1; -; Genomic DNA.  
EMBL; BC099456; AAH99456.1; -; mRNA.  
HSSP; P01270; 1ZWB.  
Ensembl; ENSMUSG0000059077; Mus musculus.  
MGI; MGI:97799; Pch.  
GO; GO:0005615; C:extracellular space; IDA.  
GO; GO:0005179; F:hormone activity; IDA.  
GO; GO:0006874; P:calcium ion homeostasis; TAS.  
InterPro; IPR001415; Parathyrd\_hrm.  
InterPro; IPR003625; Pthyrohm\_sub.  
PANTHER; PTHR10541; Pthyrohm\_sub; 1.  
Pfam; PF01279; Parathyroid; 1.  
PIRSP; PIRSF001832; PTH; 1.  
ProDom; PD010687; Pthyrohm\_sub; 1.  
SMART; SM00087; PTH; 1.  
PROSITE; PS00335; PARATHYROID; 1.  
Signal.  
SIGNAL.  
CHAIN 1 25 Potential.  
32 115 parathyroid hormone.  
SEQUENCE 115 AA; 12825 MW; DA43FABBCB4E2FD9 CRC64;  
  
Query Match 67.5%; Score 108; DB 2; Length 115;  
Best Local Similarity 71.0%; Pred. No. 2.3e-06;  
Matches 22; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 AVSEIQLMHGGGGGLNSMERVEWLRRKQLQDV 31  
|||||  
DB 32 AVSEIQLMNGLXGLASMERQWLRRKQLQDM 62  
|||||  
  
RESULT 12  
PTHY\_CHICK  
ID\_PTHY\_CHICK STANDARD; PRT; 119 AA.  
AC AC AC  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Parathyroid hormone precursor (PTH).  
GN Name=PTH.  
OS Gallus Gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
OC OC.  
NCBI\_TaxID=9031;  
[1]  
NUCLEOTIDE SEQUENCE.  
MEDLINE=89219100; PubMed=2710135;  
Russell J., Sherwood L.M.;  
"Nuclotide sequence of the DNA complementary to avian (chicken)  
preproparathyroid hormone mRNA and the deduced sequence of the hormone  
precursor.";   
Mol. Endocrinol. 3:325-331(1989).

RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=89284968; PubMed=3251402;
RA Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,
RT Kronenberg H.M.;
RT "Nucleotide sequence of cloned cDNAs encoding chicken
preparathyroid hormone.";
RL J. Bone Miner. Res. 3:689-698(1988).
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
bone and preventing their renal excretion.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
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removed.
CC
CC EMBL; M31604; AAA49093.1; -; mRNA.
DR EMBL; M36522; AAB02866.1; -; mRNA.
DR PIR; A34937; A34937.
DR HSSP; P01270; IFTY.
DR Ensembl; ENSGALG00000005358; Gallus gallus.
DR InterPro; IPR001415; Parathyroid\_hrm.
DR InterPro; IPR003626; PTH\_related.
DR InterPro; IPR003625; PTH-related.
DR PANTHER; PTHR10541; PTH-related.
DR Pfam; PF01279; Parathyroid; 1.
DR PIRSF; PIRSF001832; PTH; 1.
DR ProDom; PD013225; PTH-related; 1.
DR ProDom; PD010687; PTH-related; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 119 Parathyroid hormone.
FT
FT SQ SEQUENCE 119 AA; 13943 MW; B309D8E72997F6E CRC64;
Query Match 53.1%; Score 85; DB 1; Length 119;
Best Local Similarity 54.8%; Pred. No. 0.0027;
Matches 17; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 1 AVSEIQLMHGGGGGLNSMERVEWLKRLQDV 31
DB 32 SVSEQLMHNHVGHRHTVERQDLQKLDV 62
RESULT 13
Q6WSJ4\_FUGRU PRELIMINARY; PRT; 91 AA.
AC Q6WSJ4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Parathyroid hormone type-3.
GN Name=PTH;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI\_TaxID=31033;
RN NUCLEOTIDE SEQUENCE.
RP PubMed=14684608; DOI=10.1210/en.2003-0964;
RA Gensure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,
RA Bastepe M., Rubin D.A., Juppner H.;
RT "Identification and characterization of two parathyroid hormone-like
molecules in zebrafish.";
RL Endocrinology 145:1634-1639(2004).
DR EMBL; AY302221; AAQ73561.1; -; Genomic\_DNA.

DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007595; P:lactation; IEA.
DR InterPro; IPR001415; Parathyroid\_hrm.
DR InterPro; IPR003625; PTH-related.
DR InterPro; IPR003626; PTH-related.
DR PANTHER; PTHR10541; PTH-related.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; PTH-related; 1.
DR ProDom; PD013225; PTH-related; 2.
DR SMART; SM00087; PTH; 1.
DR SQ SEQUENCE 91 AA; 10647 MW; 75BBA25CEA64BF68 CRC64;
Query Match 42.5%; Score 68; DB 2; Length 91;
Best Local Similarity 46.7%; Pred. No. 0.38;
Matches 14; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
QY 2 VSEIQLMHGGGGGLNSMERVEWLKRLQDV 31
DB 31 ISEIQLMHNHVGHRHTVERQDLQKLDV 60
RESULT 14
CB30\_HYDMC STANDARD; PRT; 15 AA.
ID CB30\_HYDMC
AC P83630;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Chitin-binding protein HM30 (fragment).
OS Hydrangea macrophylla (Bigleaf hydrangea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; Cornales; Hydrangeaceae; Hydrangea.
OX NCBI\_TaxID=23110;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, INDUCTION, AND MASS SPECTROMETRY.
RC TISSUE=Leaf;
RX MEDLINE=21671918; PubMed=11812226; DOI=10.1006/prep.2001.1551;
RA Yang Q., Gong Z.-Z.;
RT "Purification and characterization of an ethylene-induced antifungal
protein from leaves of Guilder rose (Hydrangea macrophylla).";
RL Protein Expr. Purif. 24:76-82(2002).
CC -!- FUNCTION: Has antifungal activity against A.alternate,
A.cucumerina, A.niger, C.gossypii, F.oxysporum, F.oxysporum subsp
melonis, F.moniliforme, T.cucumeris, and V.dahliae. Has no
chitinase or agglutination activities.
CC -!- INDUCTION: By ethylene.
CC -!- MASS SPECTROMETRY: MW=30010; METHOD=Electrospray; RANGE=1-?;
CC NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC -!- CAUTION: 14 of the 15 residues are identical to an internal region
of human parathyroid hormone. That seems quite an incredible
"coincidence"
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC Antimicrobial; Chitin-binding; Direct protein sequencing; Fungicide.
KW NON\_TER 15 15
FT SQ SEQUENCE 15 AA; 1875 MW; 7EE51EECTD5B84DD CRC64;
Query Match 40.6%; Score 65; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 NSMERVEWLKRLQDV 30
DB 1 NSMERVEWLKRLQDV 15

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RESULT 15
O918E9_FUGRU
ID Q3I8E9_FUGRU PRELIMINARY; PRT; 163 AA.
AC O918E9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Parathyroid hormone-related protein precursor.
GN Name=PTHrP;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20314478; PubMed=10854780; DOI=10.1016/S0378-1119(00)00167-0;
RA Power D.M., Flannigan J., Ingleton P.M., Canario A.V.M., Danks J.,
RA Edgar G., Clark M.S.;
RT "Genomic structure and expression of parathyroid hormone-related
RL protein in a teleost, Fugu rubripes.";
RL Gene 250:67-76(2000).
DR EMBL; AJ249391; CAB94712.1; -; Genomic_DNA.
DR HSSP; P12272; IBZG
DR Ensembl; SINFRUG00000131728; Fugu rubripes.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007595; P:lactation; IEA.
DR InterPro; IPR001415; Parathyrd hrm.
DR InterPro; IPR003626; PTH_related.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD013225; PTH_related; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 163 AA; 18698 MW; 3AC5F2C764732278 CRC64;
Query Match 40.6%; Score 65; DB 2; Length 163;
Best Local Similarity 45.2%; Pred. No. 1.7;
Matches 14; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
QY 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLDV 31
Db 38 SVSHAQLMDKGRSLQEFRRRWLHLKEEV 69
Search completed: November 21, 2005, 16:15:11
Job time : 148.5 secs
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**This Page Blank (uspto)**



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 16:05:03 ; Search time 33 Seconds  
(without alignments)  
77.665 Million cell updates/sec

Title: US-09-475-158A-3

Perfect score: 160

Sequence: 1 AVSEIQLMHGGGGGLNSMERVEWLKKLQDV 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5 COMB.pep.\*

2: /cgn2\_6/ptodata/1/1aa/6 COMB.pep.\*

3: /cgn2\_6/ptodata/1/1aa/H COMB.pep.\*

4: /cgn2\_6/ptodata/1/1aa/PCRTUS COMB.pep.\*

5: /cgn2\_6/ptodata/1/1aa/RE COMB.pep.\*

6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	129	80.6	35	1	US-08-142-551B-46
2	128	80.0	33	2	US-09-447-800-6
3	128	80.0	34	2	US-09-447-800-5
4	127	79.4	34	2	US-09-044-536A-12
5	127	79.4	34	2	US-09-843-221A-17
6	127	79.4	34	2	US-09-843-221A-18
7	127	79.4	34	2	US-09-843-221A-162
8	127	79.4	34	2	US-09-843-221A-163
9	127	79.4	35	1	US-08-142-551B-52
10	127	79.4	35	1	US-08-142-551B-56
11	126	78.8	34	2	US-09-044-536A-8
12	125	78.1	31	1	US-08-262-495C-3
13	125	78.1	31	1	US-08-691-647C-1
14	125	78.1	31	1	US-08-691-647C-6
15	125	78.1	31	2	US-08-904-760B-1
16	125	78.1	31	2	US-08-904-760B-6
17	125	78.1	31	2	US-08-904-760B-14
18	125	78.1	31	2	US-08-904-760B-32
19	125	78.1	31	2	US-09-406-813-2
20	125	78.1	31	2	US-09-536-785A-1
21	125	78.1	31	2	US-09-536-785A-6
22	125	78.1	31	2	US-09-536-785A-14
23	125	78.1	31	2	US-09-536-785A-32
24	125	78.1	31	2	US-09-843-221A-27
25	125	78.1	31	2	US-09-843-221A-165
26	125	78.1	31	2	US-09-623-548A-271
27	125	78.1	31	2	US-09-657-276-271

28 125 78.1 33 2 US-09-447-800-9 Sequence 9, Appli  
29 125 78.1 34 1 US-07-765-373-1 Sequence 1, Appli  
30 125 78.1 34 1 US-08-033-099-1 Sequence 1, Appli  
31 125 78.1 34 1 US-08-262-495C-1 Sequence 1, Appli  
32 125 78.1 34 1 US-07-915-247A-1 Sequence 1, Appli  
33 125 78.1 34 1 US-08-443-863-1 Sequence 1, Appli  
34 125 78.1 34 1 US-08-448-070-1 Sequence 7, Appli  
35 125 78.1 34 1 US-08-488-105-7 Sequence 6, Appli  
36 125 78.1 34 1 US-08-468-275-6 Sequence 1, Appli  
37 125 78.1 34 1 US-08-449-500-1 Sequence 1, Appli  
38 125 78.1 34 1 US-08-449-317A-1 Sequence 2, Appli  
39 125 78.1 34 1 US-08-142-551B-2 Sequence 1, Appli  
40 125 78.1 34 1 US-08-477-022-1 Sequence 1, Appli  
41 125 78.1 34 1 US-08-449-447-1 Sequence 13, Appli  
42 125 78.1 34 1 US-08-835-231-13 Sequence 1, Appli  
43 125 78.1 34 1 US-08-184-328-1 Sequence 2, Appli  
44 125 78.1 34 1 US-08-411-726-2 Sequence 5, Appli  
45 125 78.1 34 1 US-08-691-647C-5

#### ALIGNMENTS

RESULT 1  
US-08-142-551B-46  
; Sequence 46, Application US/08142551B  
; Patent No. 5814603  
; GENERAL INFORMATION:  
; APPLICANT: Oldenburg, Kevin R.  
; APPLICANT: Selick, Harold E.  
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND  
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME  
; NUMBER OF SEQUENCES: 132  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: US  
; ZIP: 22313  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/142,551B  
; FILING DATE: 25-OCT-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/077,296  
; FILING DATE: 14-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/898,219  
; FILING DATE: 12-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/965,677  
; FILING DATE: 22-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Swiss, Gerald F.  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-010  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 854-7400  
; TELEFAX: (415) 854-8275  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 35 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Modified-site

/ LOCATION: 35  
/ OTHER INFORMATION: /note= "Where "Xaa" is selected  
/ OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine  
/ OTHER INFORMATION: anide, or the sequence of amino acids comprising  
/ OTHER INFORMATION: residues 35-84 of PTH."  
US-08-142-551B-46

Query Match 80.6%; Score 129; DB 1; Length 35;  
Best Local Similarity 80.6%; Pred. No. 5.8e-10;  
Matches 25; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGGLNSMERVEWLKRLQDV 31  
Db 1 SVSEIQLMHGGGGGLNSMERVEWLKRLQDV 31

RESULT 2

US-09-447-800-6  
/ Sequence 6, Application US/09447800  
/ Patent No. 6537965  
/ GENERAL INFORMATION:  
/ APPLICANT: BRINGHURST, F. RICHARD  
/ APPLICANT: TAKASU, HISASHI  
/ APPLICANT: GARDELLA, THOMAS J.  
/ TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)  
/ FILE OF INVENTION: ANALOGS  
/ FILE REFERENCE: 0609.4630001  
/ CURRENT APPLICATION NUMBER: US/09/447,800  
/ CURRENT FILING DATE: 1999-11-23  
/ EARLIER APPLICATION NUMBER: 60/110,152  
/ EARLIER FILING DATE: 1998-11-25  
/ NUMBER OF SEQ ID NOS: 10  
/ SOFTWARE: Patentin Ver. 2.1  
/ SEQ ID NO 6  
/ LENGTH: 33  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: MOD RES  
/ LOCATION: (1)  
/ OTHER INFORMATION: Desamino Ala  
US-09-447-800-6

Query Match 80.0%; Score 128; DB 2; Length 33;  
Best Local Similarity 87.1%; Pred. No. 7.3e-10;  
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGGLNSMERVEWLKRLQDV 31  
Db 1 AVSEIQLMHGLNKGHLNSMERVEWLKRLQDV 31

RESULT 3

US-09-447-800-5  
/ Sequence 5, Application US/09447800  
/ Patent No. 6537965  
/ GENERAL INFORMATION:  
/ APPLICANT: BRINGHURST, F. RICHARD  
/ APPLICANT: TAKASU, HISASHI  
/ APPLICANT: GARDELLA, THOMAS J.  
/ TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)  
/ FILE OF INVENTION: ANALOGS  
/ FILE REFERENCE: 0609.4630001  
/ CURRENT APPLICATION NUMBER: US/09/447,800  
/ CURRENT FILING DATE: 1999-11-23  
/ EARLIER APPLICATION NUMBER: 60/110,152  
/ EARLIER FILING DATE: 1998-11-25  
/ NUMBER OF SEQ ID NOS: 10  
/ SOFTWARE: Patentin Ver. 2.1  
/ SEQ ID NO 5  
/ LENGTH: 34  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens

/ FEATURE:  
/ NAME/KEY: MOD RES  
/ LOCATION: (1)  
/ OTHER INFORMATION: Desamino Ala  
US-09-447-800-5

Query Match 80.0%; Score 128; DB 2; Length 34;  
Best Local Similarity 87.1%; Pred. No. 7.5e-10;  
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGGLNSMERVEWLKRLQDV 31  
Db 1 AVSEIQLMHGLNKGHLNSMERVEWLKRLQDV 31

RESULT 4

US-09-044-536A-12  
/ Sequence 12, Application US/09044536A  
/ Patent No. 6025467  
/ GENERAL INFORMATION:  
/ APPLICANT: FUKUDA, Tsunehiko  
/ APPLICANT: NAKAGAWA, Shizue  
/ APPLICANT: HAKASHITA, Junko  
/ APPLICANT: TAKETOMI, Shigehisa  
/ TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE  
/ NUMBER OF SEQUENCES: 36  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
/ STREET: 130 Water Street  
/ CITY: Boston  
/ STATE: Massachusetts  
/ COUNTRY: US  
/ ZIP: 02109  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patentin Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/044,536A  
/ FILING DATE: 19-MAR-1998  
/ PRIORITY APPLICATION DATA:  
/ APPLICATION NUMBER: 08/662,871  
/ FILING DATE: 12-JUN-1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: CONLIN, David G  
/ REGISTRATION NUMBER: 27,026  
/ REFERENCE/DOCKET NUMBER: 46509-DIV  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (617)523-3400  
/ TELEFAX: (617)523-6440  
/ INFORMATION FOR SEQ ID NO: 12:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 34 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS:  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
/ FEATURE:  
/ NAME/KEY: partial peptide  
/ LOCATION: 1..34  
/ FEATURE:  
/ NAME/KEY: Modified-site  
/ LOCATION: 11  
/ OTHER INFORMATION: /product= "Xaa=Ala(2-Naph)"  
US-09-044-536A-12

Query Match 79.4%; Score 127; DB 2; Length 34;  
Best Local Similarity 83.9%; Pred. No. 1e-09;  
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGGLNSMERVEWLKRLQDV 31  
Db 1 AVSEIQLMHGLNKGHLNSMERVEWLKRLQDV 31

Db 1 SVSEIQLMHDXGKHLNSMERVWLRLKKLQDV 31

## RESULT 5

US-09-843-221A-17  
; Sequence 17, Application US/09843221A  
; Patent No. 6756480

## GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17

; LENGTH: 34

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: modified human PTH

US-09-843-221A-17

## Query Match

Best Local Similarity 79.4%; Score 127; DB 2; Length 34;

Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGLNSMERVWLRLKKLQDV 31

Db 1 SVSEIQLMNRGKHLNSMERVWLRLKKLQDV 31

## RESULT 6

US-09-843-221A-18  
; Sequence 18, Application US/09843221A  
; Patent No. 6756480

## GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18

; LENGTH: 34

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: modified human PTH

US-09-843-221A-18

## Query Match

Best Local Similarity 79.4%; Score 127; DB 2; Length 34;

Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGLNSMERVWLRLKKLQDV 31

Db 1 SVSEIQLMHNKKGHLNSMERVWLRLKKLQDV 31

## RESULT 7

US-09-843-221A-162  
; Sequence 162, Application US/09843221A  
; Patent No. 6756480

## GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 162

; LENGTH: 34

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Preferred embodiments - PTH

; NAME/KEY: misc.feature

; LOCATION: (34)..(34)

; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus

US-09-843-221A-162

## Query Match

Best Local Similarity 79.4%; Score 127; DB 2; Length 34;

Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGLNSMERVWLRLKKLQDV 31

Db 1 SVSEIQLMNRGKHLNSMERVWLRLKKLQDV 31

## RESULT 8

US-09-843-221A-163  
; Sequence 163, Application US/09843221A  
; Patent No. 6756480

## GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 163

; LENGTH: 34

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

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; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc feature
; LOCATION: (34) --(34)
; OTHER INFORMATION: Optional linker and Pc domain attached at the C-terminus
US-09-843-221A-163

Query Match      79.4%; Score 127; DB 2; Length 34;
Best Local Similarity 83.9%; Pred. No. 1e-09; 4; Indels 0; Gaps 0;
Matches 26; Conservative 1; Mismatches 0;

Qy 1 AVSEIQLMHGGGGGLNSMERVWLKKLQDV 31
Db 1 SVSEIQLMHKGKGLNSMERVWLKKLQDV 31

RESULT 9
US-08-142-551B-52
; Sequence 52, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Where "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
US-08-142-551B-52

Query Match      79.4%; Score 127; DB 1; Length 35;
Best Local Similarity 83.9%; Pred. No. 1e-09; 4; Indels 0; Gaps 0;
Matches 26; Conservative 1; Mismatches 0;

Qy 1 AVSEIQLMHGGGGGLNSMERVWLKKLQDV 31
Db 1 SVSEIQLMHKGKGLNSMERVWLKKLQDV 31
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Best Local Similarity 80.6%; Pred. No. 1e-09; 3; Indels 0; Gaps 0;
Matches 25; Conservative 3; Mismatches 3;

Qy 1 AVSEIQLMHGGGGGLNSMERVWLKKLQDV 31
Db 1 SVSEIQLMHKGKGLNSMERVWLKKLQDV 31

RESULT 10
US-08-142-551B-56
; Sequence 56, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Where "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
US-08-142-551B-56

Query Match      79.4%; Score 127; DB 1; Length 35;
Best Local Similarity 80.6%; Pred. No. 1e-09; 3; Indels 0; Gaps 0;
Matches 25; Conservative 3; Mismatches 3;

Qy 1 AVSEIQLMHGGGGGLNSMERVWLKKLQDV 31
Db 1 SVSEIQLMHKGKGLNSMERVWLKKLQDV 31
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RESULT 11  
US-09-044-536A-8  
; Sequence 8, Application US/09044536A  
; Patent No. 6025467  
; GENERAL INFORMATION:  
; APPLICANT: FUKUDA, Tsunehiko  
; APPLICANT: NAKAGAWA, Shizue  
; APPLICANT: HABASHITA, Junko  
; APPLICANT: TAKETOMI, Shigehisa  
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/044,536A  
; FILING DATE: 19-MAR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/662,871  
; FILING DATE: 12-JUN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CONLIN, David G  
; REGISTRATION NUMBER: 27,026  
; REFERENCE/DOCKET NUMBER: 46509-DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)523-3400  
; TELEFAX: (617)523-6440  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: partial peptide  
; LOCATION: 1..34  
US-09-044-536A-8  
Query Match 78.8%; Score 126; DB 2; Length 34;  
Best Local Similarity 83.9%; Pred. No. 1.4e-09;  
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 AVSEIQLMHGGGGLNSMERVEWLKRLQDV 31  
;||||||| | |||||||  
Db 1 SVSEIQLMHDKGHLNSMERVEWLKRLQDV 31  
;||||||| | |||||||  
RESULT 12  
US-08-262-495C-3  
; Sequence 3, Application US/08262495C  
; Patent No. 5556940  
; GENERAL INFORMATION:  
; APPLICANT: WILLICK, Gordon E.  
; APPLICANT: WHITFIELD, James F.  
; APPLICANT: SUREWICZ, Witold  
; APPLICANT: SUNG, wing L.  
; APPLICANT: NEUGENBAUER, Witold  
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kirby, Eades, Gale, Baker

STREET: 112 Kent Street, Suite 770,  
CITY: Ottawa  
COUNTRY: Canada  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/262,495C  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: EADES, No. 5556940ris M.  
REGISTRATION NUMBER: 5,263  
REFERENCE/DOCKET NUMBER: 36210  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (613)-237-6900  
TELEFAX: (613)-237-0045  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-262-495C-3  
Query Match 78.1%; Score 125; DB 1; Length 31;  
Best Local Similarity 83.9%; Pred. No. 1.7e-09;  
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 AVSEIQLMHGGGGLNSMERVEWLKRLQDV 31  
;||||||| | |||||||  
Db 1 SVSEIQLMHDKGHLNSMERVEWLKRLQDV 31  
;||||||| | |||||||  
RESULT 13  
US-08-691-647C-1  
; Sequence 1, Application US/08691647C  
; Patent No. 5955425  
; GENERAL INFORMATION:  
; APPLICANT: Barbier, Jean-Rene  
; APPLICANT: Morley, Paul  
; APPLICANT: Neugebauer, Witold  
; APPLICANT: Ross, Virginia  
; APPLICANT: Whitfield, James  
; APPLICANT: Willick, Gordon E.  
; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE, P.C.  
; STREET: 1100 New York Avenue, 8th Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/691,647C  
; FILING DATE: August 2, 1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Crawford, Arthur R.  
; REGISTRATION NUMBER: 25,327

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; REFERENCE/DOCKET NUMBER: 1339-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4005
; TELEFAX: (703) 816-4100
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-691-647C-1
Query Match 78.1%; Score 125; DB 1; Length 31;
Best Local Similarity 83.9%; Pred. No. 1.7e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGKGLNSMERVELRKKLDV 31
Db 1 SVSEIQLMHGKGLNSMERVELRKKLDV 31

RESULT 14
US-08-691-647C-6
; Sequence 6, Application US/08691647C
; Patent No. 5955425
; GENERAL INFORMATION:
; APPLICANT: Barbier, Jean-Rene
; APPLICANT: Morley, Paul
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE, P.C.
; STREET: 1100 New York Avenue, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; FILING DATE: August 2, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4005
; TELEFAX: (703) 816-4100
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: cyclic
; MOLECULE TYPE: protein
US-08-691-647C-6
Query Match 78.1%; Score 125; DB 1; Length 31;
Best Local Similarity 83.9%; Pred. No. 1.7e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGKGLNSMERVELRKKLDV 31
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Db 1 SVSEIQLMHGKGLNSMERVELRKKLDV 31

RESULT 15
US-08-904-760B-1
; Sequence 1, Application US/08904760B
; Patent No. 6110892
; GENERAL INFORMATION:
; APPLICANT: Jean-Rene, Barbier
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
; TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,760B
; FILING DATE: 01-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 08/691,647
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-904-760B-1
Query Match 78.1%; Score 125; DB 2; Length 31;
Best Local Similarity 83.9%; Pred. No. 1.7e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGKGLNSMERVELRKKLDV 31
Db 1 SVSEIQLMHGKGLNSMERVELRKKLDV 31

Search completed: November 21, 2005, 16:16:21
Job time : 33 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 16:15:23 ; Search time 110.5 Seconds  
(without alignments)  
117.219 Million cell updates/sec

Title: US-09-475-158A-3

Perfect score: 160

Sequence: 1 AVSEIQLMHGGGGGLNSMERVELRKLQDV 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	128	80.0	33	4	US-10-361-928-6
2	128	80.0	34	4	US-10-361-928-5
3	127	79.4	34	3	US-09-843-221A-17
4	127	79.4	34	3	US-09-843-221A-18
5	127	79.4	34	3	US-09-843-221A-162
6	127	79.4	34	3	US-09-843-221A-163
7	127	79.4	34	3	US-09-999-608-17
8	127	79.4	34	3	US-09-999-608-18
9	127	79.4	34	3	US-09-999-608-162
10	127	79.4	34	3	US-09-999-608-163
11	127	79.4	34	4	US-10-839-037-17
12	127	79.4	34	4	US-10-839-037-18
13	127	79.4	34	4	US-10-839-037-162
14	127	79.4	34	4	US-10-839-037-163
15	126	78.8	31	5	US-10-892-025-21
16	126	78.8	31	5	US-10-892-025-22
17	125	78.1	31	3	US-09-169-786-2
18	125	78.1	31	3	US-09-843-221A-27
19	125	78.1	31	3	US-09-843-221A-165
20	125	78.1	31	3	US-09-999-608-27
21	125	78.1	31	3	US-09-999-608-165
22	125	78.1	31	4	US-10-440-473-2
23	125	78.1	31	4	US-10-839-037-27
24	125	78.1	31	4	US-10-839-037-165
25	125	78.1	31	5	US-10-892-025-1
26	125	78.1	31	6	US-11-066-697-271
27	125	78.1	31	6	US-11-040-557-2

28	125	78.1	32	5	US-10-892-025-2	Sequence 2, Appli
29	125	78.1	32	6	US-11-040-557-20	Sequence 20, Appli
30	125	78.1	33	4	US-10-361-928-9	Sequence 9, Appli
31	125	78.1	33	5	US-10-892-025-3	Sequence 3, Appli
32	125	78.1	33	6	US-11-040-557-1	Sequence 1, Appli
33	125	78.1	33	6	US-11-040-557-21	Sequence 21, Appli
34	125	78.1	34	3	US-09-169-786-3	Sequence 3, Appli
35	125	78.1	34	3	US-09-858-880-5	Sequence 5, Appli
36	125	78.1	34	3	US-09-928-047B-6	Sequence 6, Appli
37	125	78.1	34	3	US-09-843-221A-16	Sequence 16, Appli
38	125	78.1	34	3	US-09-843-221A-161	Sequence 161, App
39	125	78.1	34	3	US-09-928-048A-6	Sequence 6, Appli
40	125	78.1	34	3	US-09-999-608-16	Sequence 16, App
41	125	78.1	34	3	US-09-999-608-161	Sequence 161, App
42	125	78.1	34	3	US-09-999-608-174	Sequence 174, App
43	125	78.1	34	3	US-09-999-608-175	Sequence 175, App
44	125	78.1	34	3	US-09-999-608-193	Sequence 193, App
45	125	78.1	34	4	US-10-016-403-5	Sequence 5, Appli

#### ALIGNMENTS

##### RESULT 1

US-10-361-928-6  
; Sequence 6, Application US/10361928  
; Publication No. US20030144209A1  
; GENERAL INFORMATION:  
; APPLICANT: BRINGHURST, F. RICHARD  
; APPLICANT: TAKASU, HISASHI  
; APPLICANT: GARDELLA, THOMAS J.  
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)  
; TITLE OF INVENTION: ANALOGS  
; FILE REFERENCE: 0609.4630002  
; CURRENT APPLICATION NUMBER: US/10/361,928  
; CURRENT FILING DATE: 2003-02-11  
; PRIOR APPLICATION NUMBER: 09/447,800  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: 60/110,152  
; PRIOR FILING DATE: 1998-11-25  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)-  
; OTHER INFORMATION: Desamino Ala  
US-10-361-928-6

Query Match 80.0%; Score 128; DB 4; Length 33;

Best Local Similarity 87.1%; Pred. NO. 2e-09;

Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AVSEIQLMHGGGGGLNSMERVELRKLQDV 31

DB 1 AVSEIQLMHGGGGGLNSMERVELRKLQDV 31

##### RESULT 2

US-10-361-928-5  
; Sequence 5, Application US/10361928  
; Publication No. US20030144209A1  
; GENERAL INFORMATION:  
; APPLICANT: BRINGHURST, F. RICHARD  
; APPLICANT: TAKASU, HISASHI  
; APPLICANT: GARDELLA, THOMAS J.  
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)  
; TITLE OF INVENTION: ANALOGS  
; FILE REFERENCE: 0609.4630002  
; CURRENT APPLICATION NUMBER: US/10/361,928

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; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)_
; OTHER INFORMATION: Desamino Ala
US-10-361-928-5

Query Match      80.0%; Score 128; DB 4; Length 34;
Best Local Similarity 87.1%; Pred. No. 2.1e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGGLNSMERVWLKRLQDV 31
Db 1 AVSEIQLMHNLRGKHLNSMERVWLKRLQDV 31

RESULT 3
US-09-843-221A-17
; Sequence 17, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 17
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-17
```

```
Query Match      79.4%; Score 127; DB 3; Length 34;
Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGGLNSMERVWLKRLQDV 31
Db 1 SVSEIQLMHNLRGKHLNSMERVWLKRLQDV 31
```

```
RESULT 4
US-09-843-221A-18
; Sequence 18, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
```

```
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-18

Query Match      79.4%; Score 127; DB 3; Length 34;
Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGGLNSMERVWLKRLQDV 31
Db 1 SVSEIQLMHNLRGKHLNSMERVWLKRLQDV 31

RESULT 5
US-09-843-221A-162
; Sequence 162, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 162
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc.feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-162
```

```
Query Match      79.4%; Score 127; DB 3; Length 34;
Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGGLNSMERVWLKRLQDV 31
Db 1 SVSEIQLMHNLRGKHLNSMERVWLKRLQDV 31
```

```
RESULT 6
US-09-843-221A-163
; Sequence 163, Application US/09843221A
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Query Match 79.4%; Score 127; DB 3; Length 34;  
Best Local Similarity 83.9%; Pred. No. 2.8e-09;  
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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NO. 001
US-09-999-608-162
; Sequence 162, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: GEGG, COLIN V.
; APPLICANT: JAROSINSKI, MARK ANTHONY
; APPLICANT: KINSTLER, OLAF BORIS
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
; TITLE OF INVENTION: HORMONE-RELATED PROTEIN
; FILE REFERENCE: A-665C
; CURRENT APPLICATION NUMBER: US/09/999,608
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/843,221
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 162
; LENGTH: 34

```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
;
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
; US-09-999-608-162

Query Match          79.4%; Score 127; DB 3; Length 34;
Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AVSEIQLMHGGGGGLNSMERVWLKRLQDV 31
   :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||
Db 1 SVSEIQLMHNKGKHLNSMERVWLKRLQDV 31

RESULT 10
US-09-999-608-163
; Sequence 163, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: GEGG, COLIN V.
; APPLICANT: JAROSINSKI, MARK ANTHONY
; APPLICANT: KINSTLER, OLAF BORIS
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
; TITLE OF INVENTION: HORMONE-RELATED PROTEIN
; FILE REFERENCE: A-665C
; CURRENT APPLICATION NUMBER: US/09/999,608
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/843,221
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 163
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
;
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
; US-09-999-608-163

Query Match          79.4%; Score 127; DB 3; Length 34;
Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AVSEIQLMHGGGGGLNSMERVWLKRLQDV 31
   :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||
Db 1 SVSEIQLMHNKGKHLNSMERVWLKRLQDV 31

RESULT 11
US-10-839-037-17
; Sequence 17, Application US/10839037
; Publication No. US20040214996A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
```

```
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/10/839,037
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: US/09/843,221A
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
; US-10-839-037-17

Query Match          79.4%; Score 127; DB 4; Length 34;
Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AVSEIQLMHGGGGGLNSMERVWLKRLQDV 31
   :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||
Db 1 SVSEIQLMHNKGKHLNSMERVWLKRLQDV 31

RESULT 12
US-10-839-037-18
; Sequence 18, Application US/10839037
; Publication No. US20040214996A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/10/839,037
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: US/09/843,221A
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
; US-10-839-037-18

Query Match          79.4%; Score 127; DB 4; Length 34;
Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AVSEIQLMHGGGGGLNSMERVWLKRLQDV 31
   :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||  :|||||
Db 1 SVSEIQLMHNKGKHLNSMERVWLKRLQDV 31

RESULT 13
US-10-839-037-162
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```
; Sequence 162, Application US/10839037
; Publication No. US20040214996A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/10/839,037
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: US/09/843,221A
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-10-839-037-162

Query Match      79.4%; Score 127; DB 4; Length 34;
Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      1 AVSEIQLMHGGGGGLNSMERVEWLKRLQDV 31
       :||||| | | | | | | | | | | | | | |
Db      1 SVSEIQLMHNKGLNSMERVEWLKRLQDV 31

RESULT 14
US-10-839-037-163
; Sequence 163, Application US/10839037
; Publication No. US20040214996A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/10/839,037
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: US/09/843,221A
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
```

```
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-10-839-037-163
```

```
Query Match      79.4%; Score 127; DB 4; Length 34;
Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      1 AVSEIQLMHGGGGGLNSMERVEWLKRLQDV 31
       :||||| | | | | | | | | | | | | | |
Db      1 SVSEIQLMHNKGLNSMERVEWLKRLQDV 31
```

## RESULT 15

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US-10-892-025-21
; Sequence 21, Application US/10892025
; Publication No. US20050065071A1
; GENERAL INFORMATION:
; APPLICANT: Morley, Paul
; APPLICANT: Whitfield, James F
; TITLE OF INVENTION: CYCLIC ANALOGS OF HUMAN PARATHYROID
; TITLE OF INVENTION: HORMONE FOR THE TREATMENT OF CONDITIONS CHARACTERIZED BY
; TITLE OF INVENTION: HYPERPROLIFERATIVE SKIN CELLS
; FILE REFERENCE: 3583.1000-001
; CURRENT APPLICATION NUMBER: US/10/892.025
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: 60/487,513
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1
; OTHER INFORMATION: NHR; where R is hydrogen or a linear or branched
; OTHER INFORMATION: chain alkyl, acyl or aryl group
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 13
; OTHER INFORMATION: is selected from the group consisting of Lys, Orn,
; OTHER INFORMATION: Glu, Asp, Cys, and homocysteine
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 31
; OTHER INFORMATION: Y; where Y is X, His-X, His-Asn-X, or
; OTHER INFORMATION: His-Asn-Phe-X; X is OR or NHR; and R is hydrogen
; OTHER INFORMATION: or a linear or branched chain alkyl, acyl or aryl
; OTHER INFORMATION: group
US-10-892-025-21
```

```
Query Match      78.8%; Score 126; DB 5; Length 31;
Best Local Similarity 83.9%; Pred. No. 3.5e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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```
Qy      1 AVSEIQLMHGGGGGLNSMERVEWLKRLQDV 31
       :||||| | | | | | | | | | | | | | |
Db      1 SVSEIQLMHNKGLNSMERVEWLKRLQDV 31
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Search completed: November 21, 2005, 16:34:42
Job time : 111.5 secs
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**This Page Blank (uspto)**



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; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 28
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-28

Query Match      29.1%; Score 46.5; DB 7; Length 317;
Best Local Similarity 41.4%; Pred. No. 2.8;
Matches 12; Conservative 4; Mismatches 8; Indels 5; Gaps 1;

Qy      2 VSEIOLMHGGGGLNSMERVWLKRLQD 30
Db      86 VSEADIIIVGGGYDS-----WLYGTLED 109

RESULT 3
US-10-957-569-64
; Sequence 64, Application US/10957569
; Publication No. US20050246785A1
; GENERAL INFORMATION:
; APPLICANT: COOK, Zhihong et al.
; TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
; FILE REFERENCE: 2750-1577PUS3
; CURRENT APPLICATION NUMBER: US/10/957,569
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/950,321
; PRIOR FILING DATE: 2004-09-23
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 64
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-957-569-64

Query Match      27.5%; Score 44; DB 1; Length 157;
Best Local Similarity 50.0%; Pred. No. 2.9;
Matches 8; Conservative 2; Mismatches 6; Indels 6; Gaps 0;

Qy      10 GGGGGLNSMERVWLRL 25
Db      88 GGGGGSSSRSDMKR 103

RESULT 4
US-11-074-176-256
; Sequence 256, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.

; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Ascarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256
; LENGTH: 1213
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-256

Query Match      27.5%; Score 44; DB 7; Length 1213;
Best Local Similarity 25.6%; Pred. No. 26;
Matches 11; Conservative 8; Mismatches 6; Indels 18; Gaps 1;

Qy      3 SEIQLMHGGG-----GLNSMERVWLK 27
Db      873 TSLRVPHGSGGIQDVVKVYTRAGDELSFGVNTWVKVYIAQR 915

RESULT 5
US-11-004-057-21
; Sequence 21, Application US/11004057
; Publication No. US20050244846A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Gary L.
; TITLE OF INVENTION: MEK1 PROTEINS AND FRAGMENTS THEREOF FOR USE IN REGULATING
; FILE REFERENCE: CPI-042CPPC
; CURRENT APPLICATION NUMBER: US/11/004,057
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/09/403,075
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 21
; LENGTH: 1493
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-004-057-21

Query Match      27.5%; Score 44; DB 7; Length 1493;
Best Local Similarity 27.5%; Pred. No. 32;
Matches 11; Conservative 4; Mismatches 7; Indels 18; Gaps 1;

Qy      10 GGGGGLN-----SMERVWLKRLQDV 31
Db      26 GGGGALQSGGAPAGAGULLRETGSGRERADWFRQQLRKV 65

RESULT 6
US-10-939-890-474
; Sequence 474, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
```

```

; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
; US-10-939-890-474

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Query Match      26.2%; Score 42; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 0.86;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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```

QY      7 LMHGGGGG 14
       ::::|
DB      20 ILHGGGGG 27

```

```

RESULT 7
US-10-939-890-726
; Sequence 726, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Buseat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11

```

```

; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 726
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLYATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
; US-10-939-890-726

```

```

Query Match      26.2%; Score 42; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 0.86;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 LMHGGGGG 14
       ::::|
DB      20 ILHGGGGG 27

```

```

RESULT 8
US-10-939-890-464
; Sequence 464, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Buseat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01

```

```
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 464
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-464
```

```
Query Match      25.0%; Score 40; DB 1; Length 28;
Best Local Similarity 57.1%; Pred. No. 1.6;
Matches      8; Conservative      3; Mismatches      1; Indels      1; Gaps      1;
```

```
QY      3 SEIQLMH--GGGGG 14
      ::::| | | | |
DB      14 ADQLSHFAGGGG 27
```

## RESULT 9

```
US-10-939-890-720
; Sequence 720, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Buseat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 720
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-720
```

```
QY      3 SEIQLMH--GGGGG 14
```

## US-10-939-890-720

```
Query Match      25.0%; Score 40; DB 1; Length 28;
Best Local Similarity 57.1%; Pred. No. 1.6;
Matches      8; Conservative      3; Mismatches      1; Indels      2; Gaps      1;
```

```
QY      3 SEIQLMH--GGGGG 14
      ::::| | | | |
DB      14 ADQLSHFAGGGG 27
```

## RESULT 10

```
US-10-939-890-723
; Sequence 723, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Buseat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 723
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a SATA linker
US-10-939-890-723
```

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Query Match      25.0%; Score 40; DB 1; Length 28;
Best Local Similarity 57.1%; Pred. No. 1.6;
Matches      8; Conservative      3; Mismatches      1; Indels      2; Gaps      1;
```

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QY      3 SEIQLMH--GGGGG 14
      ::::| | | | |
```





; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 340  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-131-826A-340

Query Match 24.4%; Score 39; DB 1; Length 386;  
Best Local Similarity 47.1%; Pred. No. 36;  
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 10 GGGGGLNSMERVEWLRK 26  
Db 246 GGGGPFVHRVLFRR 262

RESULT 15  
US-11-065-943-20  
; Sequence 20, Application US/11065943  
; Publication No. US20050250131A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, JEAN-LUC  
; APPLICANT: VICHIER-GUERRE, SOPHIE  
; APPLICANT: FERRIS, STEPHANE  
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I  
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES.  
; FILE REFERENCE: 266426US0XCIP  
; CURRENT APPLICATION NUMBER: US/11/065,943  
; PRIOR FILING DATE: 2005-02-25  
; PRIOR FILING DATE: 2004-02-27  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20  
; LENGTH: 562  
; TYPE: PRT  
; ORGANISM: Thermus aquaticus  
US-11-065-943-20

Query Match 24.4%; Score 39; DB 7; Length 562;  
Best Local Similarity 42.9%; Pred. No. 54;  
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 10 GGGGGLNSMERVEW 23  
Db 9 GGGGSPKALEAPW 22

Search completed: November 21, 2005, 16:34:56  
Job time : 4.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model.

Run on: November 21, 2005, 15:52:37 ; Search time 141.5 Seconds  
(without alignments)  
96.260 Million cell updates/sec

Title: US-09-475-158A-5  
Perfect score: 162  
Sequence: 1 AVSEIGGGGGGGLNLMERVEWLRKKLQDV 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 21:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162	100.0	31	3 AAY96974	Aay96974 Parathyro
2	127	78.4	31	3 AAY96973	Aay96973 Parathyro
3	116	71.6	31	3 AAY96975	Aay96975 Parathyro
4	104	64.2	89	8 ADG93251	Adg93251 Novel exp
5	103	63.6	84	2 AAR21190	Aar21190 Human par
6	103	63.6	91	8 ADF90346	Adf90346 Chimeric
7	103	63.6	91	8 ADJ87052	Adj87052 Amino aci
8	103	63.6	141	8 ADF90348	Adf90348 Chimeric
9	100	61.7	34	3 ABJ10769	Abj10769 Human par
10	100	61.7	34	3 ABJ10737	Abj10737 Human par
11	100	61.7	38	2 AAR58104	Aar58104 [Gly13]-h
12	100	61.7	38	2 AAR98958	Aar98958 Target pe
13	100	61.7	84	2 AAR21168	Aar21168 Human par
14	99	61.1	84	2 AAR23334	Aar23334 Bovine pa
15	98	60.5	34	2 AAW17939	Aaw17939 Human par
16	98	60.5	34	2 AAW67274	Aaw67274 Parathyro
17	98	60.5	34	3 ABJ10713	Abj10713 Human par
18	98	60.5	35	2 AAR74454	Aar74454 Parathyro
19	98	60.5	35	2 AAR74462	Aar74462 Parathyro
20	98	60.5	35	2 AAR74451	Aar74451 Parathyro
21	98	60.5	84	2 AAR21226	Aar21226 Human par
22	98	60.5	84	2 AAR21240	Aar21240 Human par
23	98	60.5	84	2 AAR21227	Aar21227 Human par
24	97	59.9	84	2 AAR21172	Aar21172 Human par

25	97	59.9	84	2 AAR21178	Aar21178 Human par
26	97	59.9	84	2 AAR21236	Aar21236 Human par
27	97	59.9	84	2 AAR21234	Aar21234 Human par
28	97	59.9	84	2 AAR21235	Aar21235 Human par
29	97	59.9	84	2 AAR21179	Aar21179 Human par
30	96	59.3	34	2 AAR22294	Aar22294 Human par
31	96	59.3	35	2 AAR74457	Aar74457 Parathyro
32	96	59.3	35	2 AAR74466	Aar74466 Parathyro
33	96	59.3	35	2 AAR74470	Aar74470 Parathyro
34	96	59.3	36	2 AAR58271	Aar58271 [Ala11]-h
35	96	59.3	84	2 AAR21233	Aar21233 Human par
36	96	59.3	84	2 AAR21231	Aar21231 Human par
37	96	59.3	84	2 AAR21232	Aar21232 Human par
38	96	59.3	84	2 AAR23312	Aar23312 Bovine pa
39	96	59.3	84	2 AAR21176	Aar21176 Human par
40	95	58.6	33	3 AAY98015	Aay98015 Human ami
41	95	58.6	34	2 AAR49697	Aar49697 Sequence
42	95	58.6	34	2 AAW17943	Aaw17943 Human par
43	95	58.6	34	2 AAW17941	Aaw17941 Human par
44	95	58.6	34	2 AAW67276	Aaw67276 Parathyro
45	95	58.6	34	2 AAW67278	Aaw67278 Parathyro

ALIGNMENTS

RESULT 1  
AAY96974  
ID AAY96974 standard; peptide; 31 AA.  
XX  
AC AAY96974;  
DT 31-OCT-2000 (first entry)  
XX  
DE Parathyroid hormone functional domain conjugate peptide PG9.  
XX  
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;  
KW resorption; remodeling; tether1; osteoporosis.  
XX  
OS Homo sapiens.  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT Peptide 1..5 /label= PTH N-terminal\_signaling\_domain  
FT /note= "residues 1-5"  
FT Peptide 6..14 /label= linker  
FT Peptide 15..31 /label= PTH C-terminal\_binding\_portion  
FT /note= "residues 15-31"

WO2000039278-A2.

06-JUL-2000.

30-DEC-1999; 99WO-US031108.

31-DEC-1998; 98US-0114577P.

(GARD// GARDELLA T J.

(KRON// KRONENBERG H M.

(POTT// POTTS J T.

(JUEP// JUEPPNER H.

Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

WPI; 2000-452384/39.

N-PSDB; AAAS1731.

New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.

PS Claim 7; Page 93; 119pp; English.

XX Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n

CC -R, are new, S is an amino terminal signaling functional domain of

CC parathyroid hormone (PTH); L is a linker molecule present n times (where

CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding

CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the

CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor

CC sequence. The new compounds are used for treating mammalian conditions

CC characterized by decreases in bone mass, determining rates of bone

CC reformation, bone resorption and/or bone remodeling, treating diseases

CC and disorders associated with decreased tether activity, increasing cAMP

CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or

CC non-peptide PTH (claimed). The new compound can be administered by

CC inhalation unlike the large native PTH or PTHrp which avoids the need for

CC regular injections to treat osteoporosis

XX Sequence 31 AA;

SQ Query Match 100.0%; Score 162; DB 3; Length 31;

Best Local Similarity 100.0%; Pred. NO. 8.4e-13;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSIEIGGGGGGGGGLNSMERVEWLKKLQDV 31

Db 1 AVSIEIGGGGGGGGGLNSMERVEWLKKLQDV 31

RESULT 2

AAV96973

ID AAY96973 standard; peptide; 31 AA.

XX AAY96973;

AC AAY96973;

DT 31-OCT-2000 (first entry)

XX Parathyroid hormone functional domain conjugate peptide PG5.

DE PTH; parathyroid hormone; conjugate; bone mass; bone reformation;

XX resorption; remodeling; tether; osteoporosis.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1. .9

FT /label= PTH\_N-terminal\_signaling\_domain

FT /note= "residues 1-9"

FT Peptide 10. .14

FT /label= linker

FT Peptide 15. .30

FT /label= PTH\_C-terminal\_binding\_portion

FT /note= "residues 15-31"

XX WO200039278-A2.

PN 06-JUL-2000.

PD 30-DEC-1999; 99WO-US031108.

PF 31-DEC-1998; 98US-0114577P.

PR (GARD/) GARDELLA T J.

PA (KRON/) KRONENBERG H M.

PA (POT/) POTTS J T.

PA (JUEP/) JUEPPNER H.

XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

XX WPI; 2000-452384/39.

DR N-PSDB; AAA51729.

XX

PT New compound comprising an amino terminal signaling functional domain

PT linked to a carboxy-terminal binding portion of parathyroid hormone for

PT treating mammalian conditions characterized by decreases in bone mass.

XX Claim 7; Page 92-93; 119pp; English.

PS Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n

CC -R, are new, S is an amino terminal signaling functional domain of

CC parathyroid hormone (PTH); L is a linker molecule present n times (where

CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding

CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the

CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor

CC sequence. The new compounds are used for treating mammalian conditions

CC characterized by decreases in bone mass, determining rates of bone

CC reformation, bone resorption and/or bone remodeling, treating diseases

CC and disorders associated with decreased tether activity, increasing cAMP

CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or

CC non-peptide PTH (claimed). The new compound can be administered by

CC inhalation unlike the large native PTH or PTHrp which avoids the need for

CC regular injections to treat osteoporosis

XX Sequence 31 AA;

SQ Query Match 78.4%; Score 127; DB 3; Length 31;

Best Local Similarity 87.1%; Pred. NO. 1.7e-08;

Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AVSIEIGGGGGGGGGLNSMERVEWLKKLQDV 31

Db 1 AVSIEIQLMHGGGGGGLNSMERVEWLKKLQDV 31

RESULT 3

AAV96975

ID AAY96975 standard; peptide; 31 AA.

XX AAY96975;

AC AAY96975;

DT 31-OCT-2000 (first entry)

XX Parathyroid hormone functional domain conjugate peptide PG7.

DE PTH; parathyroid hormone; conjugate; bone mass; bone reformation;

XX resorption; remodeling; tether; osteoporosis.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1. .9

FT /label= PTH\_N-terminal\_signaling\_domain

FT /note= "residues 1-9"

FT Peptide 10. .16

FT /label= linker

FT Peptide 17. .31

FT /label= PTH\_C-terminal\_binding\_portion

FT /note= "residues 17-31"

XX WO200039278-A2.

PN 06-JUL-2000.

PD 30-DEC-1999; 99WO-US031108.

PF 31-DEC-1998; 98US-0114577P.

PR (GARD/) GARDELLA T J.

PA (KRON/) KRONENBERG H M.

PA (POT/) POTTS J T.

PA (JUEP/) JUEPPNER H.

XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

XX WPI; 2000-452384/39.

DR N-PSDB; AAA51729.

XX

DR WPI; 2000-452384/39.  
 DR N-PSDB; AAA51730.  
 XX New compound comprising an amino terminal signaling functional domain  
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
 PT treating mammalian conditions characterized by decreases in bone mass.  
 XX  
 PS Claim 7; Page 93; 119pp; English.  
 XX  
 CC Compounds of the structure or formula S-(L)<sub>n</sub>-B, R<sub>1</sub>-S-(L)<sub>n</sub>-R or S-(L)<sub>n</sub>-  
 CC -R, are new. S is an amino terminal signaling functional domain of  
 CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
 CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
 CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R<sub>1</sub> is the  
 CC PTH-1 receptor signal sequence; and R is a (a portion of) PTH-1 receptor  
 CC sequence. The new compounds are used for treating mammalian conditions  
 CC characterized by decreases in bone mass, determining rates of bone  
 CC reformation, bone resorption and/or bone remodeling, treating diseases  
 CC and disorders associated with decreased tether activity, increasing cAMP  
 CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
 CC non-peptide PTH (claimed). The new compound can be administered by  
 CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
 CC regular injections to treat osteoporosis  
 XX  
 SQ Sequence 31 AA;  
 Query Match 71.6%; Score 116; DB 3; Length 31;  
 Best Local Similarity 77.1%; Pred. No. 3.9e-07;  
 Matches 27; Conservative 0; Mismatches 0; Indels 8; Gaps 2;  
 Oy 1 AVSEI---GGGGGGGGGLNSMERVEWLKRLQDV 31  
 Db 1 AVSEIQLMHGGGGGGG-----SMERVEWLKRLQDV 31  
 RESULT 4  
 ADG93251  
 ID ADG93251 standard; protein; 89 AA.  
 XX  
 AC ADG93251;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Novel expression cassette encoded amino acid sequence SeqID132.  
 XX  
 KW expression cassette; high yield polypeptide production;  
 KW tandem polypeptide; inclusion body.  
 XX  
 OS Unidentified.  
 OS Synthetic.  
 XX  
 PN WO2003100021-A2.  
 XX  
 PD 04-DEC-2003.  
 XX  
 XX 23-MAY-2003; 2003WO-US016643.  
 XX  
 XX 24-MAY-2002; 2002US-0383370P.  
 XX  
 XX (REST-) RESTORAGEN INC.  
 PA (HARL/) HARLEY S.  
 XX  
 XX Harley S, Williams JA, Luan P, Xia Y;  
 PI  
 DR WPI; 2004-035128/03.  
 DR N-PSDB; ADG93252.  
 XX  
 XX New expression cassette comprising an operably linked nucleic acid  
 PT sequence, useful for producing a tandem polypeptide that forms an  
 PT inclusion body when expressed in a cell.  
 XX  
 PS Example 6; SEQ ID NO 132, 157pp; English.  
 XX

CC This invention relates to a novel expression cassette and methods for  
 CC high yield production of polypeptides. The cassette comprises an operably  
 CC linked nucleic acid sequence, where the expression of the cassette  
 CC produces a tandem polypeptide that forms an inclusion body when expressed  
 CC in a cell. The expression cassette is useful for producing peptide and  
 CC polypeptide in a cell, preferably a tandem polypeptide that forms an  
 CC inclusion body when expressed in a cell. The present sequence is that of  
 CC an amino acid sequence encoded by an expression cassette of the  
 CC invention.  
 XX  
 SQ Sequence 89 AA;  
 Query Match 64.2%; Score 104; DB 8; Length 89;  
 Best Local Similarity 59.0%; Pred. No. 3.3e-05;  
 Matches 23; Conservative 1; Mismatches 3; Indels 12; Gaps 1;  
 Oy 5 IGGGGGG-----GGGLNSMERVEWLKRLQDV 31  
 Db 48 VGGGGGPRSVSEIQLMFNLGHLNSMERVEWLKRLQDV 86  
 RESULT 5  
 AAR21190  
 ID AAR21190 standard; protein; 84 AA.  
 XX  
 AC AAR21190;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 17-JUN-1992 (first entry)  
 XX  
 DE Human parathyroid hormone analogue, [Ala1Gly6]hPTH.  
 XX  
 KW PTH; agonist; antagonist; receptor binding.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9200753-A.  
 XX  
 PD 23-JAN-1992.  
 XX  
 PF 13-JUL-1990; 90US-00553760.  
 XX  
 PR 13-JUL-1990; 90US-00553760.  
 XX  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX Cohen PA, Nissenson RA, Strewler GJ;  
 PI  
 DR WPI; 1992-056643/07.  
 XX  
 PT New modified parathyroid hormone analogues - useful in treating cancer,  
 PT osteoporosis, hypercalcaemia and hyper-parathyroid conditions.  
 XX  
 PS Claim 15; Page 64; 86pp; English.  
 XX  
 XX Residues 35-84 may be absent. The C-terminal gp. may be -COOH, -COO-M  
 CC (M+ = cation), or -(C=O)NH2. 140 specific peptides derived from human PTH  
 CC are given in the specification (AAR21150-256, AAR23226- 3250 + AAR23522-  
 CC 529). Corresp. peptides created using residues 7-84 of bovine and porcine  
 CC PTH are also claimed. All have mutations at positions 3, and/or 6, and/or  
 CC 9 which result in surface side chains which are useful to modulate  
 CC receptor binding and activity. They are useful as agonists and  
 CC antagonists in the treatment of conditions or diseases involving PTH.  
 CC The peptides are pref. prepd. by solid phase synthesis. See also AAR21257  
 CC (human generic), AAR21258 (bovine generic) and AAR21259 (porcine  
 CC generic). (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 84 AA;  
 Query Match 63.6%; Score 103; DB 2; Length 84;  
 Best Local Similarity 77.4%; Pred. No. 4.1e-05;  
 Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AVSEIGGGGGGGGGLNSMERVEWLKQLQDV 31  
 |||||  
 Db 1 AVSEIGLHNLGKHLNSMERVEWLKQLQDV 31

## RESULT 6

ID ADF90346 standard; protein, 91 AA.  
 AC ADF90346;  
 DT 26-FEB-2004 (first entry)  
 DE Chimeric protein SEQ ID NO:19.  
 XX  
 XX  
 XX  
 KW A palladium complex-promoted hydrolytic polypeptide cleavage;  
 KW Cys-His cleavage site; palladium promoter; chimeric protein;  
 KW inclusion body.  
 XX  
 XX  
 OS Synthetic.  
 OS  
 XX  
 XX  
 PN WO2003100015-A2.  
 XX  
 PD 04-DEC-2003.  
 XX  
 XX  
 XX  
 PF 23-MAY-2003; 2003WO-US016468.  
 XX  
 PR 24-MAY-2002; 2002US-0383488P.  
 XX  
 XX (REST-) RESTORAGEN INC.  
 PA  
 XX  
 XX  
 PI Seo JS, Strydom D, Holmquist B;  
 XX  
 XX WPI; 2004-053266/05.  
 DR N-PSDB; ADF90345.  
 DR  
 XX  
 XX  
 PT A palladium complex-promoted hydrolytic polypeptide cleavage process for  
 PT cleaving the polypeptide at a Cys-His cleavage site, comprises  
 PT solubilizing the polypeptide in mixture of a palladium promoter dissolved  
 PT in organic acid solvent.  
 XX  
 XX  
 PS Example 9; SEQ ID NO 19; 56pp; English.

XX The present invention describes a palladium complex-promoted hydrolytic  
 CC polypeptide cleavage process, which selectively cleaves the polypeptide  
 CC at a Cys-His cleavage site. The process comprises solubilizing the  
 CC polypeptide in a reaction mixture comprised of a palladium promoter  
 CC dissolved in a high-concentration organic acid solvent. Also described:  
 CC (1) a peptide purification process; and (2) a process for producing a  
 CC peptide. The methods are useful for selectively cleaving the polypeptide  
 CC at Cys-His cleavage site. The process provides a highly specific,  
 CC conformationally independent, palladium promoted hydrolytic cleavage of  
 CC polypeptides, including cleavage of relatively insoluble chimeric  
 CC proteins in the form of inclusion bodies. The present sequence is used in  
 CC the exemplification of the present invention.

SQ Sequence 91 AA;

Query Match 63.6%; Score 103; DB 8; Length 91;  
 Best Local Similarity 56.1%; Pred. No. 4.4e-05;  
 Matches 23; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 5 IGGGGG-----GGGLNSMERVEWLKQLQDV 31  
 :|||||  
 Db 48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLKQLQDV 88  
 :|||||

## RESULT 7

ADJ87052 standard; protein, 91 AA.

XX  
 AC ADJ87052;  
 XX

DT 06-MAY-2004 (first entry)

XX Amino acid sequence of chimeric protein T7tag-Vg-GSpr-CH-pth(1-34).

XX growth hormone releasing factor; GRF; hydrolytic polypeptide cleavage;  
 KW palladium promoter; formic acid; inclusion body; glucagon like peptide-1;  
 KW GLP-1; GLP-2; parathyroid hormone; PTH;  
 KW parathyroid hormone related hormone; adrenocorticotrophic hormone; ACTH;  
 KW enkephalins; endorphin; exendin; amylin; opioid peptide; gaegurin 5;  
 KW gaegurin 6; brevinin 1; ranatuerin; esculentin;  
 KW glucose dependent insulinotropic polypeptide; GIP; glucagon; motilin;  
 KW thymopoietin; thymosin; ubiquitin; serum thymic factor;  
 KW thymic humoral factor; neurotensin; tuftsin; gastrin; calcitonin;  
 KW luteinising hormone releasing hormone; pancreatic polypeptide;  
 KW endothelin; corticotropin releasing factor; neuropeptide Y;  
 KW atrial natriuretic peptide; amylin; galanin; somatostatin;  
 KW vasoactive intestinal peptide; insulin; chimera.

OS Chimeric.  
 OS Synthetic.

XX WO2004011599-A2.

XX 05-FEB-2004.

XX 23-MAY-2003; 2003WO-US016647.

XX 24-MAY-2002; 2002US-0383484P.

XX (REST-) RESTORAGEN INC.

XX Seo JS, Holmquist B;

XX WPI; 2004-203533/19.

DR N-PSDB; ADJ87051.

XX Hydrolytic polypeptide cleavage process useful for selectively cleaving  
 PT the polypeptide at the Cys-His cleavage site, comprises solubilizing the  
 PT polypeptide in a reaction mixture containing a palladium promoter  
 PT dissolved in formic acid.

XX Claim 11; Fig 5; 41pp; English.

XX The present sequence represents chimeric protein T7tag-Vg-GSpr-CH-pth(1-  
 CC 34). The protein comprises parathyroid hormone (PTH). The chimeric  
 CC protein is used to demonstrate the process of the invention. The  
 CC specification describes a hydrolytic polypeptide cleavage process which  
 CC selectively cleaves the polypeptide at the Cys-His cleavage site. The  
 CC process comprises solubilizing the polypeptide in a reaction mixture  
 CC containing a palladium promoter dissolved in formic acid. The polypeptide  
 CC is in the form of an inclusion body, and is preferably glucagon like  
 CC peptide-1 (GLP-1), GLP-2, growth hormone releasing factor (GRF),  
 CC parathyroid hormone (PTH), parathyroid hormone related hormone,  
 CC adrenocorticotrophic hormone (ACTH), enkephalins, endorphins, exendins,  
 CC amylin, various opioid peptides, gaegurin 5, gaegurin 6, brevinin 1,  
 CC ranatuerin 1-9, an esculentin, glucose dependent insulinotropic  
 CC polypeptide (GIP), glucagon, motilin, thymopoietin, thymosin, ubiquitin,  
 CC serum thymic factor, thymic humoral factor, neurotensin, tuftsin,  
 CC gastrin, calcitonin, luteinising hormone releasing hormone, pancreatic  
 CC polypeptide, endothelin, corticotropin releasing factor, neuropeptide Y,  
 CC atrial natriuretic peptide, amylin, galanin, somatostatin, vasoactive  
 CC intestinal peptide or insulin. The process is highly specific, and is not  
 CC affected by the polypeptide sequence or the size of the cleaved peptide  
 CC product.

XX Sequence 91 AA;

Query Match 63.6%; Score 103; DB 8; Length 91;  
 Best Local Similarity 56.1%; Pred. No. 4.4e-05;  
 Matches 23; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 5 IGGGGG-----GGGLNSMERVEWLKQLQDV 31  
 :|||||

Db 48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVWLRLKKLQDV 88

## RESULT 8

ADP90348  
ID ADF90348 standard; protein; 141 AA.

AC ADF90348;

XX 26-FEB-2004 (first entry)

DT 26-FEB-2004 (first entry)

DE Chimeric protein SEQ ID NO:21.

XX palladium complex-promoted hydrolytic polypeptide cleavage;

KW Cys-His cleavage site; palladium promoter; chimeric protein;

KW inclusion body.

XX Synthetic.

OS WO2003100015-A2.

PN 04-DEC-2003.

XX 23-MAY-2003; 2003WO-US016468.

PD 24-MAY-2002; 2002US-0383488P.

XX (REST-) RESTORAGEN INC.

PI Seo JS, Strydom D, Holmquist B;

XX WPI; 2004-053266/05.

DR N-PSDB; ADF90347.

XX A palladium complex-promoted hydrolytic polypeptide cleavage process for

PT cleaving the polypeptide at a Cys-His cleavage site, comprises

PT solubilizing the polypeptide in mixture of a palladium promoter dissolved

PT in organic acid solvent.

XX Example 11; SEQ ID NO 21; 56pp; English.

XX The present invention describes a palladium complex-promoted hydrolytic

CC polypeptide cleavage process, which selectively cleaves the polypeptide

CC at a Cys-His cleavage site. The process comprises solubilising the

CC polypeptide in a reaction mixture comprised of a palladium promoter

CC dissolved in a high-concentration organic acid solvent. Also described:

CC (1) a peptide purification process; and (2) a process for producing a

CC peptide. The methods are useful for selectively cleaving the polypeptide

CC at Cys-His cleavage site. The process provides a highly specific,

CC conformationally independent, palladium promoted hydrolytic cleavage of

CC polypeptides, including cleavage of relatively insoluble chimeric

CC proteins in the form of inclusion bodies. The present sequence is used in

CC the exemplification of the present invention.

XX Sequence 141 AA;

SQ

Query Match 63.6%; Score 103; DB 8; Length 141;

Best Local Similarity 56.1%; Pred. No. 6.8e-05;

Matches 23; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

DE Human parathyroid hormone analogue #65.

XX Human; parathyroid hormone; parathyroid hormone-related protein; PTH;

KW PTHrP; analogue; abnormal CNS function; pancreatic function;

KW mineral metabolism; male infertility; abnormal blood pressure;

KW hypothalamic disease.

XX Homo sapiens.

OS Synthetic.

XX Key

FT Modified-site 7

FT /label= OTHER

FT /note= "OTHER=cyclohexylalanine"

FT Modified-site 8

FT /label= OTHER

FT /note= "OTHER=des-Met"

FT Modified-site 9

FT /label= OTHER

FT /note= "OTHER=des-His"

FT Modified-site 10

FT /label= OTHER

FT /note= "OTHER=des-Asn"

FT Modified-site 11

FT /label= OTHER

FT /note= "OTHER=cyclohexylalanine"

FT Modified-site 34

FT /note= "C-terminal amide"

XX WO9957139-A2.

PN 11-NOV-1999.

XX 03-MAY-1999; 99WO-US009521.

XX 05-MAY-1998; 98US-00072956.

XX (SCRC) SOC CONSEILS RECH & APPL SCI.

XX Choev M, Dong ZX, Rosenblatt M;

XX WPI; 2000-038790/03.

XX New parathyroid hormone analogs, used for treating e.g. abnormal CNS or

CC pancreatic functions, abnormal mineral metabolism and homeostasis, male

CC infertility, abnormal blood pressure or hypothalamic disease.

XX Claim 11; Page 39; 49pp; English.

XX The present invention provides a number of parathyroid hormone (PTH) or

CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2

CC receptor agonists or antagonists and can be used in the treatment of

CC disorders resulting from altered or excessive action of the PTH2

CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,

CC divergence from normal mineral metabolism and homeostasis, male

DE

XX

KW

KW

KW

XX

XX

OS

XX

FT

FT

FT

FT

FT

FT

FT

FT

XX

XX

XX

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XX

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XX

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XX

XX

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XX

XX

XX

XX

Query Match 61.7%; Score 100; DB 3; Length 34;

Best Local Similarity 71.0%; Pred. No. 3.9e-05;

Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 AVSEITGGGGGGGGLNSMERVWLRLKKLQDV 31

Db 1 SVSEITQXXXXXGKHLNSMERVWLRLKKLQDV 31

RESULT 10

ABJ10737

ID ABJ10737 standard; peptide; 34 AA.

XX

AC ABJ10737;  
XX  
DT 02-DEC-2002 (first entry)  
XX  
XX Human parathyroid hormone analogue #33.  
DE Human; parathyroid hormone; parathyroid hormone-related protein; PTH;  
XX PTHrP; analogue; abnormal CNS function; pancreatic function;  
KW mineral metabolism; male infertility; abnormal blood pressure;  
KW hypothalamic disease.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
PH Key Location/Qualifiers  
FI Modified-site 7  
FI /label= OTHER  
FI /note= "OTHER-cyclohexylalanine"  
FT Modified-site 8  
FT /label= OTHER  
FT /note= "OTHER-des-Met"  
FT Modified-site 11  
FT /label= OTHER  
FT /note= "OTHER-cyclohexylalanine"  
FT Modified-site 34  
FT /note= "C-terminal amide"  
FT  
XX WO9557139-A2.  
XX  
XX 11-NOV-1999.  
XX  
XX 03-MAY-1999; 99WO-US009521.  
XX  
XX 05-MAY-1998; 98US-00072956.  
XX  
XX (SCRC ) SOC CONSELS RECH & APPL SCI.  
XX  
XX Chorev M, Dong ZX, Rosenblatt M;  
XX WPI; 2000-038790/03.  
XX  
XX New parathyroid hormone analogs, used for treating e.g. abnormal CNS or  
PT pancreatic functions; abnormal mineral metabolism and homeostasis, male  
PT infertility, abnormal blood pressure or hypothalamic disease.  
XX  
XX Claim 11; Page 39; 49pp; English.  
XX  
XX The present invention provides a number of parathyroid hormone (PTH) or  
CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2  
CC receptor agonists or antagonists and can be used in the treatment of  
CC disorders resulting from altered or excessive action of the PTH2  
CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,  
CC divergence from normal mineral metabolism and homeostasis, male  
CC infertility, abnormal blood pressure or a hypothalamic disease. The  
CC present sequence is a peptide analogue of the invention  
XX  
SQ Sequence 34 AA;  
Query Match 61.7%; Score 100; DB 3; Length 34;  
Best Local Similarity 71.0%; Pred. No. 3.9e-05;  
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
QY 1 AVSEIGGGGGGGGGLNSMERVWLRLKQLQDV 31  
Db 1 SVSEIQXHNKXGHLNSMERVWLRLKQLQDV 31  
RESULT 11  
AAR58104  
XX AAR58104 standard; peptide; 38 AA.  
XX  
XX AAR58104;  
XX

DT 20-SEP-1994 (first entry)  
XX [Gly13]-hPTH(1-38)-OH.  
XX Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;  
KW fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.  
XX Synthetic.  
OS  
PN GB2269176-A.  
XX  
XX 02-FEB-1994.  
XX  
XX 12-JUL-1993; 93GB-00014384.  
XX  
XX 15-JUL-1992; 92GB-00015009.  
PR 18-DEC-1992; 92GB-00026415.  
PR 23-DEC-1992; 92GB-00026859.  
PR 23-DEC-1992; 92GB-00028861.  
PR 28-JAN-1993; 93GB-00001691.  
PR 28-JAN-1993; 93GB-00001692.  
PR 14-APR-1993; 93GB-00007673.  
PR 19-APR-1993; 93GB-00008033.  
XX (SANO ) SANDOZ LTD.  
XX  
XX Lewis I, Schneider H, Waelchli R, Rainer A;  
PI WPI; 1994-018352/03.  
XX  
XX New active para-thyroid hormone variants - used for treating or  
PT preventing osteoporosis etc.  
XX  
XX Example 101; Page 39; 92pp; English.  
XX  
XX This peptide is an example of a highly generic formula covering  
CC parathyroid hormone variants useful for treating or preventing bone  
CC conditions associated with calcium depletion/resorption, in cases where  
CC calcium fixation is required (esp. osteoporosis) or to treat  
CC hypoparathyroidism  
XX  
SQ Sequence 38 AA;  
Query Match 61.7%; Score 100; DB 2; Length 38;  
Best Local Similarity 74.2%; Pred. No. 4.4e-05;  
Matches 23; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
QY 1 AVSEIGGGGGGGGGLNSMERVWLRLKQLQDV 31  
Db 1 SVSEIQLMNHLGHLNSMERVWLRLKQLQDV 31  
RESULT 12  
AAR98958  
ID AAR98958 standard; peptide; 38 AA.  
XX  
XX AAR98958;  
XX  
XX 15-JAN-1997 (first entry)  
DT  
XX Target peptide (PTH(1-38)) used in fusion protein construct.  
DE  
XX Fusion protein construct; isolation; purification;  
KW growth hormone releasing factor; glucagon-like peptide 1;  
KW Parathyroid hormone; inclusion body; carbonic anhydrase.  
XX  
XX Synthetic.  
OS  
XX WO9617942-A1.  
PN  
XX 13-JUN-1996.  
PD  
XX 07-DEC-1995; 95WO-US015800.  
PF



```
XX 07-DEC-1994; 94US-00350530.
XX (BION-) BIONEERASKA INC.
XX Partridge BE, Stout JS, Henriksen DB, Manning SD, De La Motte RS;
XX Holmquist B, Wagner FW;
XX WPI; 1996-287186/29.
XX
XX Isolation and purifcn of peptide(s) from fusion protein constructs -
XX which include a carbonic anhydrase and a variable fused polypeptide.
XX
XX Claim 58; Page 50; 67pp; English.
XX
XX A new method for the isolation and/or purification of a recombinant
XX peptide employs a fusion protein construct (FPC) comprising a carbonic
XX anhydrase and a variable fused polypeptide containing a target peptide.
XX The method comprises precipitating either the FPC or a fragment of the
XX FPC including the carbonic anhydrase. An alternative method of producing
XX the peptide comprises expressing the FPC as part of an inclusion body.
XX The target peptides of the FPC are derived from growth hormone releasing
XX factor (GRF), glucagon-like peptide 1 (GLP1) or parathyroid hormone
XX (PTH). This sequence corresponds to amino acids 1-38 of PTH
XX
XX Sequence 38 AA;
XX
XX Query Match 61.7%; Score 100; DB 2; Length 38;
XX Best Local Similarity 74.2%; Pred. No. 4.4e-05;
XX Matches 23; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
XX
XX QY 1 AVSEIGGGGGGGGLNSMERVEWLRLKKLDV 31
XX :||||| | ||||| ||||| |||||
XX Db 1 SVSEIGLMLNGLKHLNSMERVEWLRLKKLDV 31
XX
XX RESULT 13
XX AAR21168
XX ID AAR21168 standard; protein; 84 AA.
XX AC AAR21168;
XX
XX 25-MAR-2003 (revised)
XX 17-JUN-1992 (first entry)
XX
XX Human parathyroid hormone analogue, [Gly6]hPTH.
XX
XX PTH; agonist; antagonist; receptor binding.
XX
XX Synthetic.
XX
XX WO9200753-A.
XX
XX 23-JAN-1992.
XX
XX 13-JUL-1990; 90US-00553760.
XX
XX 13-JUL-1990; 90US-00553760.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Cohen FA, Nissenson RA, Strewler GJ;
XX
XX WPI; 1992-056643/07.
XX
XX New modified parathyroid hormone analogues - useful in treating cancer,
XX osteoporosis, hypercalcaemia and hyper-parathyroid conditions.
XX
XX Claim 15; Page 64; 86pp; English.
XX
XX Residues 35-84 may be absent. The C-terminal gp. may be -COOH, -COO-+M
XX (M+ = cation), or -(C=O)NH2. 140 specific peptides derived from human PTH
XX are given in the specification (AAR21150-256, AAR23226- 3250 + AAR23522-
XX
XX 07-DEC-1994; 94US-00350530.
XX (BION-) BIONEERASKA INC.
XX Partridge BE, Stout JS, Henriksen DB, Manning SD, De La Motte RS;
XX Holmquist B, Wagner FW;
XX WPI; 1996-287186/29.
XX
XX Isolation and purifcn of peptide(s) from fusion protein constructs -
XX which include a carbonic anhydrase and a variable fused polypeptide.
XX
XX Claim 58; Page 50; 67pp; English.
XX
XX A new method for the isolation and/or purification of a recombinant
XX peptide employs a fusion protein construct (FPC) comprising a carbonic
XX anhydrase and a variable fused polypeptide containing a target peptide.
XX The method comprises precipitating either the FPC or a fragment of the
XX FPC including the carbonic anhydrase. An alternative method of producing
XX the peptide comprises expressing the FPC as part of an inclusion body.
XX The target peptides of the FPC are derived from growth hormone releasing
XX factor (GRF), glucagon-like peptide 1 (GLP1) or parathyroid hormone
XX (PTH). This sequence corresponds to amino acids 1-38 of PTH
XX
XX Sequence 38 AA;
XX
XX Query Match 61.7%; Score 100; DB 2; Length 84;
XX Best Local Similarity 74.2%; Pred. No. 9.6e-05;
XX Matches 23; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
XX
XX QY 1 AVSEIGGGGGGGGLNSMERVEWLRLKKLDV 31
XX :||||| | ||||| ||||| |||||
XX Db 1 SVSEIGLMLNGLKHLNSMERVEWLRLKKLDV 31
XX
XX RESULT 14
XX AAR23334
XX ID AAR23334 standard; protein; 84 AA.
XX AC AAR23334;
XX
XX 25-MAR-2003 (revised)
XX 22-JUN-1992 (first entry)
XX
XX Bovine parathyroid hormone analogue, [Gly6]bPTH.
XX
XX PTH; agonist; antagonist; receptor binding.
XX
XX Synthetic.
XX
XX WO9200753-A.
XX
XX 23-JAN-1992.
XX
XX 13-JUL-1990; 90US-00553760.
XX
XX 13-JUL-1990; 90US-00553760.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Cohen FA, Nissenson RA, Strewler GJ;
XX
XX WPI; 1992-056643/07.
XX
XX New modified parathyroid hormone analogues - useful in treating cancer,
XX osteoporosis, hypercalcaemia and hyper-parathyroid conditions.
XX
XX Claim 15; Page 64; 86pp; English.
XX
XX Residues 35-84 may be absent. The C-terminal gp. may be -COOH, -COO-+M
XX (M+ = cation), or -(C=O)NH2. 142 specific peptides derived from bovine
XX PTH are given in the specification (AAR23251-382, and AAR23540-549).
XX
XX Corresp. peptides created using residues 7-84 of human and porcine PTH
XX are also claimed. All have mutations at positions 3, and/or 6, and/or 9
XX which result in surface side chains which are useful to modulate receptor
XX binding and activity. They are useful as agonists and antagonists in the
XX treatment of conditions or diseases involving PTH. The peptides are
XX pref. prepd. by solid phase synthesis. See also AAR21257 (human generic),
XX AAR21258 (bovine generic) and AAR21259 (porcine generic). (Updated on 25-
XX MAR-2003 to correct PA field.)
XX
XX Sequence 84 AA;
XX
XX Query Match 61.1%; Score 99; DB 2; Length 84;
XX Best Local Similarity 74.2%; Pred. No. 0.00013;
XX Matches 23; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
XX
XX QY 1 AVSEIGGGGGGGGLNSMERVEWLRLKKLDV 31
```

Search completed: November 21, 2005, 16:10:12  
Job time : 142.5 secs

Db 1 AVSEIGFMHNLGKHLSSMERVEWLRKKLDV 31

RESULT 15  
AAW17939  
ID AAW17939 standard; peptide; 34 AA.  
AC AAW17939;  
XX  
DT 29-JUL-1997 (first entry)  
XX  
DE Human parathyroid hormone analogue [Cha7,11]hPTH(1-34)NH2.  
XX  
KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;  
XX bone fracture.  
XX  
OS Homo sapiens.  
OS Synthetic.

XX Key Location/Qualifiers  
FT Modified-site 7  
FT /label= OTHER  
FT /note= "Cyclohexylalanine (Cha)"  
FT Modified-site 11  
FT /label= OTHER  
FT /note= "Cha"  
FT Modified-site 34  
FT /note= "In amide form"

XX WO9702834-A1.  
XX  
XX 30-JAN-1997.  
XX  
XX 03-JUL-1996; 96WO-US011292.  
XX  
XX 13-JUL-1995; 95US-0001105P.  
XX 06-SEP-1992; 95US-0003305P.  
XX 23-MAR-1996; 96US-00626186.  
XX  
XX (BIOM-) BIONEASURE INC.  
XX  
XX Dong ZX;  
XX WPI; 1997-118819/11.  
XX  
XX New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis and bone fracture.

XX Claim 5; Page; 33pp; English.  
XX  
XX The present sequence is a specific example of a human parathyroid hormone (hPTH) analogue from fragment 1-34 in which at least one of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31 is cyclohexylalanine (Cha). In this example the Leu residue at position 7 and the Leu at position 11 in the wild-type have been substituted by Cha. The hPTH analogues stimulate bone growth and so are useful in human or veterinary medicine for treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and calcitonin). N.B. The present sequence does not appear in the specification. It corresponds to the known hPTH 1-34 fragment with the modifications as stated in the claim

XX Sequence 34 AA;  
XX  
XX Query Match 60.5%; Score 98; DB 2; Length 34;  
XX Best Local Similarity 71.0%; Fred. No. 6.9e-05;  
XX Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 AVSEIGGGGGGGGLNSMERVEWLRKKLDV 31  
Db 1 SVSEIQMHXGKHLNSMERVEWLRKKLDV 31

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 16:05:13 ; Search time 23.5 Seconds  
(without alignments)  
126.924 Million cell updates/sec

Title: US-09-475-158A-5

Perfect score: 162

Sequence: 1 AVSBIIGGGGGGGLNSMERVELRKKLQDV 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	56.8	115	1 PTHU	parathyroid hormon
2	91	56.2	115	1 PTHO	parathyroid hormon
3	88	54.3	115	2 JC4202	parathyroid hormon
4	84	51.9	115	1 PTPG	parathyroid hormon
5	77	47.5	115	2 A05091	parathyroid hormon
6	72	44.4	105	2 I51851	parathyroid hormon
7	66	40.7	1336	2 T18288	ABC transport prot
8	64	39.5	212	2 T49559	related to proline
9	64	39.5	440	2 S71795	transcription fact
10	64	39.5	543	2 A41211	early growth respo
11	63.5	39.2	644	2 A53184	myc far upstream e
12	63	38.9	425	2 T03605	probable DNA bindi
13	63	38.9	1090	2 A41696	regulatory protein
14	63	38.9	1428	2 T13926	probable protein p
15	63	38.9	1596	2 A33106	neurogenic locus m
16	63	38.9	1858	2 T18273	1-phosphatidylinos
17	62.5	38.6	644	1 I40712	endo-1,4-beta-xyla
18	62	38.3	252	2 T45737	hypothetical prote
19	62	38.3	486	2 C96699	hypothetical prote
20	61.5	38.0	415	2 D96664	hypothetical prote
21	61.5	38.0	1047	2 G87398	AcRb/AcrD/AcrF fam
22	61.5	38.0	1066	2 G84746	hypothetical prote
23	61	37.7	199	2 T49450	hypothetical prote
24	61	37.7	199	2 S16063	acp-22 protein - y
25	61	37.7	199	2 S32224	acp-22 protein - y
26	61	37.7	201	2 T49792	hypothetical prote
27	61	37.7	209	2 D86399	protein F17L21.18
28	61	37.7	594	2 B86456	protein trihelix D
29	61	37.7	649	2 S58064	hdc protein - frui

#### RESULT 1

PTHU

parathyroid hormone precursor [validated] - human

N:Alternate names: parathyroid hormone

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence revision 19-Jan-1996 #text change 09-Jul-2004

C:Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90387; A90426; A94410; I38

R:Vasicsek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J.T.

Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983

A:Title: Nucleotide sequence of the human parathyroid hormone gene.

A:Reference number: A19339; MUID:83169834; PMID:6220408

A:Accession: A19339

A:Molecule type: DNA

A:Residues: 1-115 <V>

A:Cross-references: UNIPROT:P01270; UNIPARC:UPI000013290A; GB:J00301; NID:G190702; PIDN

R:Yanaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.

Biol. Chem. Hoppe-Seyler 375, 821-824, 1994

A:Title: Purification of meprin from human kidney and its role in parathyroid hormone de

A:Reference number: S53790; MUID:95225988; PMID:7710697

A:Accession: S53790

A:Molecule type: protein

A:Residues: 'X', 33, 'X', 35-46; 65-84; 105-110 <Y>

A:Cross-references: UNIPARC:UPI00001734E1; UNIPARC:UPI00001734E2; UNIPARC:UPI00001734E3

A>Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also occur

R:Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.

Nature 249, 155-157, 1974

A:Title: Structural analysis of human parathyroid hormone by a new microsequencing ai

A:Reference number: A93169; MUID:74174967; PMID:4833516

A:Accession: A93169

A:Molecule type: protein

A:Residues: 26-37 <J>

A:Cross-references: UNIPARC:UPI00001734E4

R:Olstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik, V.

Eur. J. Biochem. 205, 311-319, 1992

A:Title: Isolation and characterization of two biologically active O-glycosylated forms

ation.

A:Reference number: S21199; MUID:92209518; PMID:1555591

A:Accession: S21199

A:Molecule type: protein

A:Residues: 32-114, 'N' <OLS>

A:Cross-references: UNIPARC:UPI00001734E5

A>Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylation

R:Niall, H.D.; Sauer, R.T.; Jacoba, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L.H

Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974

A:Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyroid

A:Reference number: A93789; MUID:74111656; PMID:4521809

A:Accession: A93789

A:Molecule type: protein

A:Residues: 32-68 <NIA>

A:Cross-references: UNIPARC:UPI000002DA05

R:Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D.

Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

A;Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal residues 1-31  
A;Reference number: A93783; MUID:73070429; PMID:4509319  
A;Accession: A93783  
A;Molecule type: protein  
A;Residues: 32-52,'Q',54-58,'K',60,'L',62-65 <BRE>  
A;Cross-references: UNIPARC:UPI00001734E6  
R;Keutmann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.  
Biochemistry 14, 1842-1847, 1975  
A;Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone.  
A;Reference number: A90387; MUID:75146516; PMID:1125201  
A;Accession: A90387  
A;Molecule type: protein  
A;Residues: 52-75 <KE3>  
A;Cross-references: UNIPARC:UPI00001734E7  
R;Keutmann, H.T.; Sauer, M.W.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.  
Biochemistry 17, 5723-5729, 1978  
A;Title: Complete amino acid sequence of human parathyroid hormone.  
A;Reference number: A90426; MUID:79082855; PMID:728431  
A;Accession: A90426  
A;Molecule type: protein  
A;Residues: 61-106,'D',108-115 <KEU>  
A;Cross-references: UNIPARC:UPI00001734E8  
R;Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.  
in Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9-10  
A;Reference number: A94410  
A;Accession: A94410  
A;Molecule type: protein  
A;Residues: 75-100 <KE2>  
A;Cross-references: UNIPARC:UPI00001734E9  
R;Tregear, G.W.; van Riettschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J.  
Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974  
A;Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of human parathyroid hormone.  
A;Reference number: A91660; MUID:75059220; PMID:4474131  
A;Contents: annotation; synthesis of residues 32-65  
A;Note: the biologically active amino-terminal 34 residues of parathyroid hormone were synthesized by solid-phase methods and characterized by biological assays in the chick at renal adenylate cyclase assay and with the bovine hormone's active region in the chick.  
R;Andreatta, R.A.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Riniker, B.; Rittel, H.; Chapp, A.C. 56, 470-473, 1973  
A;Title: Synthese der Sequenz 1-34 von menschlichem Parathormon.  
A;Reference number: A91635; MUID:74227467; PMID:4721748  
A;Contents: annotation; synthesis of residues 32-65  
A;Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined in chorioepitheloidectomized rats caused a distinct increase in plasma calcium level  
R;Hendy, G.N.; Kronenberg, H.M.; Potts, J.T.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981  
A;Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.  
A;Reference number: I38342; MUID:82150870; PMID:6950381  
A;Accession: I38342  
A;Status: translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-115 <RES>  
A;Cross-references: UNIPARC:UPI000013290A; EMBL:V00597; NID:g37143; PIDN:CAA23843.1; PIDN:CAA23439.1  
C;Genetics:  
A;Gene: GDB:PTH  
A;Cross-references: GDB:119522; OMIM:168450  
A;Map position: 11p15.2-11p15.1  
A;Introns: 29/2  
A;Note: the first intron occurs before the initiator codon  
C;Function:  
A;Description: factor in homeostatic control of plasma calcium and phosphate; released by parathyroid gland  
C;Superfamily: parathyroid hormone; parathyroid hormone homology  
C;Keywords: calcium; hormone; parathyroid gland; plasma  
F;1-25/Domain: signal sequence #status predicted <SIG>  
F;26-31/Domain: propeptide #status experimental <PRO>  
F;30-64/Domain: parathyroid hormone homology <PTH>  
F;32-115/Product: parathyroid hormone #status experimental <MAT>  
Query Match 56.8%; Score 92; DB 1; Length 115;  
Best Local Similarity 71.0%; Pred. No. 0.00047;  
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

RESULT 2  
PTBO  
parathyroid hormone precursor - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 23-Oct-1981 #sequence revision 23-Oct-1981 #text change 09-Jul-2004  
A;Accession: A24949; A93935; A93773; A91648; A93773; I45975; I45976; A01534  
R;Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.  
Gene 28, 319-329, 1984  
A;Title: Isolation and complete nucleotide sequence of the gene for bovine parathyroid hormone.  
A;Reference number: A24949; MUID:84262483; PMID:6086460  
A;Accession: A24949  
A;Molecule type: DNA  
A;Residues: 1-115 <WEA>  
A;Cross-references: UNIPROT:P01268; UNIPARC:UPI0000132907; GB:K01938  
R;Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; Potts Jr., J.T.  
Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979  
A;Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid hormone.  
A;Reference number: A93835; MUID:80056617; PMID:388425  
A;Accession: A93835  
A;Molecule type: DNA  
A;Residues: 1-115 <KRO>  
A;Cross-references: UNIPARC:UPI0000132907; GB:V00106; GB:J00023; NID:984; PIDN:CAA23439.1  
A;Note: the authors translated the codon GAA for residue 50 as Gly  
R;Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn, D.V.  
Proc. Natl. Acad. Sci. U.S.A. 71, 653-656, 1974  
A;Title: The N-terminal amino-acid sequence of bovine parathyroid hormone.  
A;Reference number: A93793; MUID:74142666; PMID:4522780  
A;Accession: A93793  
A;Molecule type: protein  
A;Residues: 26-115 <HAM>  
A;Cross-references: UNIPARC:UPI00001734DF  
R;Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; Dawson, B.F.; Aurbach, G.D.; Potts Jr., J.T.; Cohn, D.V.  
Hoppe-Seyler's Z. Physiol. Chem. 351, 1586-1588, 1970  
A;Title: The amino acid sequence of bovine parathyroid hormone I.  
A;Reference number: A91648; MUID:71076162; PMID:5531031  
A;Accession: A91648  
A;Molecule type: protein  
A;Residues: 32-115 <NIA>  
A;Cross-references: UNIPARC:UPI00000473E4  
R;Brewer Jr., H.B.; Ronan, R.  
Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970  
A;Title: Bovine parathyroid hormone: amino acid sequence.  
A;Reference number: A93773; MUID:71063634; PMID:5275384  
A;Accession: A93773  
A;Molecule type: protein  
A;Residues: 32-115 <BRE>  
A;Cross-references: UNIPARC:UPI00000473E4  
R;Potts Jr., J.T.; Tregear, G.W.; Keutmann, H.T.; Niall, H.D.; Sauer, R.; Deftos, L.J.; Potts Jr., J.T.  
Proc. Natl. Acad. Sci. U.S.A. 68, 63-67, 1971  
A;Title: Synthesis of a biologically active N-terminal tetraoctapeptide of parathyroid hormone.  
A;Reference number: A93776; MUID:71091588; PMID:4322265  
A;Contents: annotation; synthesis of residues 32-65  
A;Note: the synthetic peptide was active in vivo and in vitro  
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littlejohn, T.; Arnaud, C.D.  
Am. J. Med. 56, 759-766, 1974  
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone.  
A;Reference number: A90030; MUID:74173303; PMID:4598526  
A;Contents: annotation  
R;Weaver, C.A.; Gordon, D.F.  
Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981  
A;Title: Introduction by molecular cloning of artificial inverted sequences at the 5' telomere of the parathyroid hormone gene.  
A;Reference number: I45975; MUID:82037785; PMID:6170060  
A;Accession: I45975  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-115 <WE2>  
A;Cross-references: UNIPARC:UPI0000132907; GB:J00024; NID:g163642; PIDN:AAA30747.1; PIDN:CAA23439.1  
R;Weaver, C.A.; Gordon, D.F.

Biochemistry 14, 3631-3635, 1975  
A;Title: Porcine parathyroid hormone. Identification, biosynthesis, and partial amino acid sequence.  
A;Reference number: A90390; MUID:76018954; PMID:1164500  
A;Accession: A90390  
A;Molecule type: protein  
A;Residues: 26-115 <CHU>  
A;Cross-references: UNIPARC:UPI00001592DF  
R;Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr., J.  
Biochemistry 13, 1994-1999, 1974  
A;Title: The amino acid sequence of porcine parathyroid hormone.  
A;Reference number: A90376; MUID:74253317; PMID:4840833  
A;Accession: A90376  
A;Molecule type: protein  
A;Residues: 32-109 <SAU>  
A;Cross-references: UNIPARC:UPI00001734E0  
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.  
Am. J. Med. 56, 759-766, 1974  
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone.  
A;Reference number: A90030; MUID:74173303; PMID:4598526  
A;Contents: annotation  
C;Superfamily: parathyroid hormone; parathyroid hormone homology  
C;Keywords: calcium; hormone; parathyroid gland  
F;1-25/Domain: signal sequence #status predicted <SIG>  
F;26-31/Domain: propeptide #status experimental <PRO>  
F;30-64/Domain: parathyroid hormone homology <PTH>  
F;32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 51.9%; Score 84; DB 1; Length 115;  
Best Local Similarity 64.5%; Pred. No. 0.0041;  
Matches 20; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 AVSEITGGGGGGGGLNSMERVWLRLKQLQDV 31  
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Db 32 SVSEIQLMHNLGKHLSSLERVWLRLKQLQDV 62

RESULT 5  
A05091  
parathyroid hormone precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-Jul-2004  
C;Accession: A05091; A26806  
R;Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.  
J. Biol. Chem. 259, 3320-3329, 1984  
A;Reference number: A05091; MUID:84135846; PMID:6321505  
A;Accession: A05091  
A;Molecule type: DNA  
A;Residues: 1-115 <HEI>  
A;Cross-references: UNIPROT:P04089; UNIPARC:UPI000013290C; GB:X01268; NID:G206483; PIDN:  
A;Note: the authors translated the codon GAA for residue 87 as Asp  
R;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.  
Nucleic Acids Res. 15, 6740, 1987  
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hor.  
A;Reference number: A26806; MUID:87316938; PMID:3628009  
A;Accession: A26806  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-115 <SCH>  
A;Cross-references: UNIPARC:UPI000013290C; GB:X05721; GB:Y00409; NID:G56002; PIDN:CAA29  
C;Genetics:  
A;Introns: 29/3  
C;Superfamily: parathyroid hormone; parathyroid hormone homology  
F;30-64/Domain: parathyroid hormone homology <PTH>

Query Match 47.5%; Score 77; DB 2; Length 115;  
Best Local Similarity 61.3%; Pred. No. 0.028;  
Matches 19; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 AVSEITGGGGGGGGLNSMERVWLRLKQLQDV 31  
:||||| :|:|||||  
Db 32 AVSEIQLMHNLGKHLASVERMQLRLKQLQDV 62



Mol. Cell. Biol. 11, 5735-5745, 1991

A;Molecule type: alkene  
A:Residues: 1-1596 <SMO>

A;Molecule type: alkene  
A:Residues: 1-1596 <SMO>

A;Cross-references: UNIPROT:P21519; UNIPARC:UPI000012EB74; GB:X54251; NID:g8203; PIDN:CA  
A;Note: strain Canton S  
C;Genetics:  
A;Gene: FlyBase:mam  
A;Cross-references: FlyBase:FBgn0002643  
Query Match 38.9%; Score 63; DB 2; Length 1596;  
Best Local Similarity 84.6%; Pred. NO. 16;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 5 TGGGGGGGGGLNS 17  
Db 354 VGGGGGGGGGNS 366  
Search completed: November 21, 2005, 16:17:16  
Job time : 24.5 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 15:55:27 ; Search time 146.5 Seconds  
(without alignments)  
149.293 Million cell updates/sec

Title: US-09-475-158A-5  
Perfect score: 162  
Sequence: 1 AVSBIGGGGGGGGLNSMERVELRKKLQDV 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	56.8	115	1 PTHY_HUMAN	P01270 homo sapien
2	92	56.8	115	1 PTHY_WACFA	Q9xt35 macaca faec
3	92	56.8	115	2 Q4VB48_HUMAN	Q4vb48 homo sapien
4	91	56.2	115	1 PTHY_BOVIN	P01268 bos taurus
5	88	54.3	86	2 Q9N1V0_HORSE	P52212 canis famil
6	88	54.3	115	1 PTHY_CANFA	P01269 sus scrofa
7	84	51.9	115	1 PTHY_PIG	Q9gl67 felis silve
8	81	50.0	115	1 PTHY_PELCA	Q80w22 rattus norv
9	77	47.5	105	2 Q80WZ2_RAT	P04089 rattus norv
10	77	47.5	115	1 PTHY_RAT	Q92016 mus musculu
11	75	46.3	115	2 Q920L6_MOUSE	P53349 mus musculu
12	73.5	45.4	1493	1 M3K1_MOUSE	Q6k708 oryza sativ
13	70.5	43.5	770	2 Q6K708_ORYSA	P6t5k2 oryza sativ
14	70.5	43.5	836	2 Q6T5K2_ORYSA	Q944ul oryza sativ
15	70.5	43.5	836	2 Q944U1_ORYSA	Q78su3 neurospora
16	70	43.2	565	2 Q4IQD8_GIBZE	Q4iqd8 gibberella
17	70	43.2	581	2 Q4IQD8_GIBZE	Q5krj6 corynebacte
18	69.5	42.9	1596	2 Q5KRJ6_CORGL	Q8ln95 oryza sativ
19	69	42.6	138	2 Q8LN95_ORYSA	Q6pf28 xenopus lae
20	69	42.6	913	2 Q6PF28_XENLA	Q94h89 oryza sativ
21	68.5	42.3	420	2 Q94H89_ORYSA	Q691l7 oryza sativ
22	68	42.0	444	2 Q691L7_ORYSA	Q73627 anolis caro
23	68	42.0	454	2 Q73627_ANOCA	Q5n802 oryza sativ
24	68	42.0	481	2 Q5N802_ORYSA	Q7pyh7 anopheles g
25	68	42.0	555	2 Q7PYH7_ANOGA	Q55s19 cryptococcu
26	68	42.0	591	2 Q55S19_CRYNE	Q5kgnl cryptococcu
27	68	42.0	591	2 Q5KGHL_CRYNE	Q6mjti bdellovibri
28	67.5	41.7	325	2 Q6MJTI_BDEBA	Q59mn9 candida alb
29	67.5	41.7	524	2 Q59MN9_CANAL	Q7s5t5 neurospora
30	67	41.4	425	2 Q7S5T5_NEUCR	Q62004 branchiosto
31	67	41.4	620	2 Q62004_BRAFL	

32 67 41.4 634 2 Q54UJ4\_DICDI Q54uj4 dictyosteli  
33 67 41.4 836 2 Q8GST0\_ORYSA Q8gst0 oryza sativ  
34 67 41.4 959 2 Q561P7\_CRYNE Q561p7 cryptococcu  
35 67 41.4 985 2 Q5KQ88\_CRYNE Q5kq88 cryptococcu  
36 66.5 41.0 137 2 Q69K54\_ORYSA Q69k54 oryza sativ  
37 66.5 41.0 531 2 Q9SOK7\_ARATH Q9sok7 arabidopsais  
38 66.5 41.0 822 2 Q7XCT3\_ORYSA Q7xct3 oryza sativ  
39 66.5 41.0 822 2 Q94HZ3\_ORYSA Q94hz3 oryza sativ  
40 66 40.7 362 2 Q6Z2M3\_ORYSA Q6z2m3 oryza sativ  
41 66 40.7 422 2 Q96755\_BRALA Q96755 branchiosto  
42 66 40.7 559 2 Q54Y02\_DICDI Q54y02 dictyosteli  
43 66 40.7 637 2 Q75HJ0\_ORYSA Q75hj0 oryza sativ  
44 66 40.7 766 2 Q4SGK9\_TETNG Q4sgk9 tetraodon n  
45 66 40.7 1513 2 Q559C0\_DICDI Q559c0 dictyosteli

## ALIGNMENTS

RESULT 1  
PTHY\_HUMAN STANDARD; PRT; 115 AA.  
AC P01270;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).  
GN Name=PTH;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;  
RT "Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone."  
RL Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Vasicek T.J., McCevitt B.E., Freeman M.W., Fennick B.J., Hendy G.N., Potts J.T. Jr., Rich A., Kronenberg H.M.;  
RT "Nucleotide sequence of the human parathyroid hormone gene."  
RL Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).  
RN [3]  
RP PROTEIN SEQUENCE OF 26-37.  
RA Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;  
RT "Structural analysis of human parathyroid hormone by a new microsequencing approach."  
RL Nature 249:155-157(1974).  
RN [4]  
RP PROTEIN SEQUENCE OF 26-40.  
RA PubMed=15340161; DOI=10.1110/ps.04682504;  
RT Zhang Z., Henzel W.J.;  
RT "Signal peptide prediction based on analysis of experimentally verified cleavage sites."  
RL Protein Sci. 13:2819-2824(2004).  
RN [5]  
RP PROTEIN SEQUENCE OF 32-68.  
RA Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V., O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;  
RT "The amino-acid sequence of the amino-terminal 37 residues of human parathyroid hormone."  
RL Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).  
RN [6]  
RP PROTEIN SEQUENCE OF 61-83 AND 84-115.  
RA MEDLINE=79082855; PubMed=728431;  
Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,

RA Potts J.T. Jr.;  
RT "Complete amino acid sequence of human parathyroid hormone.";  
RL Biochemistry 17:5723-5729(1978).  
RN [7]  
RP PROTEIN SEQUENCE OF 75-100.  
RA Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,  
RL O'Riordan J.L.H., Potts J.T. Jr.;  
RA (In) Talmadge R.V., Owen M., Parsons J.A. (eds.);  
RL Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation,  
RL Amsterdam (1975).  
RN [8]  
RP SEQUENCE REVISION. PubMed=1125201;  
RX MEDLINE=75146316;  
RA Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;  
RT "A reinvestigation of the amino-terminal sequence of human parathyroid  
RL hormone.";  
RL Biochemistry 14:1842-1847(1975).  
RN [9]  
RP SYNTHESIS OF 32-65.  
RX MEDLINE=75059220; PubMed=4474131;  
RA Tregear G.W., van Rietshoeten J., Green E., Niall H.D., Keutmann H.T.,  
RA Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;  
RT "Solid-phase synthesis of the biologically active N-terminal 1-34  
RL peptide of human parathyroid hormone.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).  
RN [10]  
RP SYNTHESIS OF 32-65.  
RX MEDLINE=73227467; PubMed=4721748;  
RA Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,  
RA Riniker B., Rittel W., Sieber P.;  
RT "Synthesis of sequence 1-34 of human parathyroid hormone.";  
RL Helv. Chim. Acta 56:470-473(1973).  
RN [11]  
RP STRUCTURE BY NMR OF 32-65.  
RX MEDLINE=91299748; PubMed=2069952;  
RA Klaus W., Diekmann T., Wray V., Schomburg D., Wingender E., Mayer H.;  
RT "Investigation of the solution structure of the human parathyroid  
RL hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry, and  
RL molecular dynamics calculations.";  
RL Biochemistry 30:6936-6942(1991).  
RN [12]  
RP STRUCTURE BY NMR OF 32-65.  
RX MEDLINE=93345518; PubMed=8344299;  
RA Barden J.A., Cuthbertson R.M.;  
RT "Stabilized NMR structure of human parathyroid hormone (1-34).";  
RL Eur. J. Biochem. 215:315-321(1993).  
RN [13]  
RP STRUCTURE BY NMR OF 32-68.  
RX MEDLINE=95318084; PubMed=7797503; DOI=10.1074/jbc.270.25.15194;  
RA Marx U.C., Auestermann S., Bayer P., Adermann K., Eichart A.,  
RA Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,  
RA Roesch P.;  
RT "Structure of human parathyroid hormone 1-37 in solution.";  
RL J. Biol. Chem. 270:15194-15202(1995).  
RN [14]  
RP STRUCTURE BY NMR OF 32-70.  
RX MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;  
RA Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Roesch P.;  
RT "Solution structures of human parathyroid hormone fragments hPTH(1-34)  
RL and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";  
RL Biochem. Biophys. Res. Commun. 267:213-220(2000).  
RN [15]  
RP VARIANT PTH ARG-18.  
RX MEDLINE=91009811; PubMed=2212001;  
RA Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,  
RA Kronenberg H.M.;  
RT "Mutation of the signal peptide-encoding region of the  
RL preproparathyroid hormone gene in familial isolated  
RL hypoparathyroidism.";  
RL J. Clin. Invest. 86:1084-1087(1990).  
RN [16]  
RP VARIANT PTH PRO-23.  
RX PubMed=10523031;  
Query Match 56.8%; Score 92; DB 1; Length 115;  
RA EMBL; J00301; AAA60215.1; -, Genomic\_DNA.  
RT EMBL; V00597; CA23843.1; -, mRNA.  
RL EMBL; A29146; CA01956.1; -, Unassigned\_DNA.  
RN PIR; A19339; PTHU.  
RP PDB; 1BW; NMR; @=32-70.  
RT PDB; 1ET1; X-ray; A/B=32-65.  
RL PDB; 1ET2; Model; A=32-65.  
RN PDB; 1FV; NMR; @=32-65.  
RT PDB; 1HPH; NMR; @=32-65.  
RL PDB; 1HPV; NMR; @=32-65.  
RN PDB; 1HTH; NMR; @=32-65.  
RT PDB; 1ZWA; NMR; @=32-65.  
RL PDB; 1ZWB; NMR; @=33-68.  
RN PDB; 1ZWD; NMR; @=34-68.  
RT PDB; 1ZWE; NMR; @=35-68.  
RL PDB; 1ZWF; NMR; @=35-68.  
RN PDB; 1ZWG; NMR; @=35-68.  
RT Ensembl; ENSG00000152266; Homo sapiens.  
RL HGNC; HGNC:9606; PTH.  
RN MIM; 168450; -.  
RP GO; GO:000576; C:extracellular region; NAS.  
RT GO; GO:0005179; F:hormone activity; TAS.  
RL GO; GO:0045453; P:bone resorption; NAS.  
RN GO; GO:0006874; P:calcium ion homeostasis; NAS.  
RT GO; GO:0046058; P:cAMP metabolism; TAS.  
RL GO; GO:0007267; P:cell-cell signaling; TAS.  
RN GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.  
RT GO; GO:0008628; P:induction of apoptosis by hormones; TAS.  
RL InterPro; IPR001501; P:skeletal development; TAS.  
RN InterPro; IPR003625; P:thyroid\_hrm.  
RT PANTHER; PTHR10541; P:thyroid\_sub; 1.  
RL Pfam; PF01279; Parathyroid; 1.  
RN PIRSF; PIRSF001832; PTH; 1.  
RT SMART; SM00087; P:thyroid\_sub; 1.  
RN PROSITE; PS00335; PARATHYROID; 1.  
KW 3D-structure, Direct protein sequencing; Disease mutation; Hormone;  
RN SIGNAL. 1 25 Parathyroid hormone.  
RT PROPEP 26 31 C->R (in PTH, dominant; leads to  
RL CHAIN 32 115 inefficient processing of the precursor).  
RN VARIANT 18 18 /FTID=VAR\_006047  
RT VARIANT 23 23 S\_P (in PTH, recessive, might lead to  
FT CONFLICT 107 107 /FTID=VAR\_018464.  
FT HELIX 34 64 N -> D (in Ref. 6).  
FT SEQUENCE 115 AA; 12861 MW; 849015736A6E5597 CRC64;  
SQ

DE	10-MAY-2005 (Ver. 4), Last annotation update!
DT	Parathyroid hormone precursor (Parathyrin) (PTH).
DI	
DR	Name=PTH;
GS	Bos taurus (Bovine).
GN	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC	Pecora; Bovidae; Bovinae; Bos.
OX	NCBI_TaxID=9913;
	[1]
RP	NCLEOTIDE SEQUENCE.
RP	
RX	MEDLINE=80056617;PubMed=388425;

RA Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,  
RA Potts J.T. Jr., Rich A.;  
RT "Cloning and nucleotide sequence of DNA coding for bovine  
RT preproparathyroid hormone.";  
RN Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).  
RN (2).  
RP NUCLEOTIDE SEQUENCE  
RX MEDLINE=882037785; PubMed=6170060;  
RA Weaver C.A., Gordon D.F., Kemper B.;  
RT "Introduction by molecular cloning of artifactual inverted sequences  
RT at the 5' terminus of the sense strand of bovine parathyroid hormone  
RT cDNA.";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).  
RN (3).  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=83105964; PubMed=6185374; DOI=10.1016/0303-7207(82)90136-8;  
RA Weaver C.A., Gordon D.F., Kemper B.;  
RT "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";  
RL Mol. Cell. Endocrinol. 28:411-424(1982).  
RN (4).  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=84262483; PubMed=6086460; DOI=10.1016/0378-1119(84)90149-5;  
RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;  
RT "Isolation and complete nucleotide sequence of the gene for bovine  
RT parathyroid hormone.";  
RL Gene 28:319-329(1984).  
RN (5).  
RP PROTEIN SEQUENCE OF 26-115.  
RX MEDLINE=74142666; PubMed=4522780;  
RA Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,  
RA Conn D.V.;  
RT "The N-terminal amino-acid sequence of bovine parathyroid  
RT hormone.";  
RL Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).  
RN (6).  
RP PROTEIN SEQUENCE OF 32-115.  
RX MEDLINE=71076162; PubMed=5531031;  
RA Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,  
RA Aurbach G.D., Potts J.T. Jr.;  
RT "The amino acid sequence of bovine parathyroid hormone I.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).  
RN (7).  
RP PROTEIN SEQUENCE OF 32-115.  
RX MEDLINE=71063634; PubMed=5275384;  
RA Brewer H.B. Jr., Ronan R.;  
RT "Bovine parathyroid hormone: amino acid sequence.";  
RL Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).  
RN (8).  
RP SYNTHESIS OF 32-65.  
RX MEDLINE=71091588; PubMed=4322265;  
RA Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,  
RA Defcos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;  
RT "Synthesis of a biologically active N-terminal tetra-  
RT of parathyroid hormone.";  
RL Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).  
RN (9).  
RP STRUCTURE BY NMR OF 32-68.  
RX MEDLINE=20090619; PubMed=40623601; DOI=10.1006/bbrc.1999.1958;  
RA Marx U.C., Ademann K., Bayer P., Forssmann W.-G., Rosch P.;  
RT "Solution structures of human parathyroid hormone fragments hPTH(1-34)  
RT and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";  
RL Biochem. Biophys. Res. Commun. 267:213-220(2000).  
CC -1- FUNCTION: PTH elevates calcium level by dissolving the salts in  
CC bone and preventing their renal excretion.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the parathyroid hormone family.  
CC -----  
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CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----

DR EMBL; V00106; CAA23439.1; -; mRNA.  
DR EMBL; J00024; AAA30747.1; -; mRNA.  
DR EMBL; K01938; AAA30749.1; -; Genomic\_DNA.  
DR EMBL; M25082; AAA30748.1; -; mRNA.  
DR PIR; A24949; PTBO.  
DR PDB; 1ZWC; NMR; @=32-68.  
DR InterPro; IPR001415; Parathyroid\_hrm.  
DR InterPro; IPR003625; Pthyrrhorm\_sub.  
DR PANTHER; PTHR10541; Pthyrrhorm\_sub; 1.  
DR Pfam; PF01279; Parathyroid; 1.  
DR PIRSF; PIRSF001832; PTH; 1.  
DR ProDom; PD010687; Pthyrrhorm\_sub; 1.  
DR SMART; SM00087; PTH; 1.  
DR PROSITE; PS00335; PARATHYROID; 1.  
KW 3D-structure; Direct protein sequencing; Hormone; Signal.  
FT SIGNAL 1 25  
FT PROPEP 26 31 Parathyroid hormone.  
FT CHAIN 32 115 V -> G (in Ref. 4).  
FT CONFLICT 106 106  
FT HELIX 37 40  
FT TURN 41 42  
FT TURN 51 52  
FT HELIX 53 60  
FT TURN 61 63  
SQ SEQUENCE 115 AA; 12980 MW; 2ED245B348880710 CRC64;  
  
Query Match 56.2%; Score 91; DB 1; Length 115;  
Best Local Similarity 71.0%; Pred. NO. 0.0041;  
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 AVSEIGGGGGGGGINSERVEWLRKLLQDV 31  
DB 32 AVSEIQFMHNLGKHLSSMERVEWLRKLLQDV 62  
  
RESULT 5  
QNIV0 HORSE  
ID Q9NIV0 HORSE PRELIMINARY; PRT; 86 AA.  
AC Q9NIV0;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Parathyroid hormone (Fragment).  
GN Name=PTH;  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20082971; PubMed=10613847; DOI=10.1101/gr.9.12.1239;  
RA Caetano A.R., Shue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,  
RA Bowling A.T., Murray J.D.;  
RT "A comparative gene map of the horse (Equus caballus).";  
RL Genome Res. 9:1239-1249(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Shue Y.-L., Caetano A.R., Lyons L.A., O'Brien S.J., Laughlin T.F.,  
RA Murray J.D., Bowling A.T.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF134233; AAF62347.1; -; Genomic\_DNA.  
DR HSSP; P01270; IFT1.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0005179; F:hormone activity; IEA.  
DR InterPro; IPR001415; Parathyroid\_hrm.  
DR InterPro; IPR003625; Pthyrrhorm\_sub.  
DR PANTHER; PTHR10541; Pthyrrhorm\_sub; 1.  
DR Pfam; PF01279; Parathyroid; 1.  
DR ProDom; PD010687; Pthyrrhorm\_sub; 1.  
DR SMART; SM00087; PTH; 1.  
DR PROSITE; PS00335; PARATHYROID; 1.  
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Query Match 54.3%; Score 88; DB 2; Length 86;  
Best Local Similarity 67.7%; Pred. No. 0.0069;  
Matches 21; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 AVSIEIGGGGGGGGGLNSMERVWLRLKLDV 31  
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DB 3 SVSEIQMHNLGKHLNSMERVWLRLKLDV 33

## RESULT 6

PTHY\_CANFA STANDARD; PRT; 115 AA.  
AC P52212;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Parathyroid hormone precursor (Parathyrin) (PTH).  
GN Name=PTH;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
OC Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Parathyroid;  
RX MEDLINE=95369696; PubMed=7642102; DOI=10.1016/0378-1119(94)00912-C;  
RA Rosol T.J., Steinmeyer C.L., McCauley L.K., Greene A., Dewille J.W.,  
RA Capen C.C.;  
RT "Sequences of the cDNAs encoding canine parathyroid hormone-related  
protein and parathyroid hormone."  
RL Gene 160:241-243(1995).  
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in  
CC bone and preventing their renal excretion.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; U15662; AA82584.1; -; mRNA.  
DR PIR; JC4202; JC4202.  
DR HSP; P01268; 12WC.  
DR Ensembl; ENSCAFG00000008177; Canis familiaris.  
DR InterPro; IPR001415; Parathyrd hrm.  
DR InterPro; IPR003625; Pthyrdorm sub.  
DR PANTHER; PTHR10541; Pthyrdorm sub; 1.  
DR Pfam; PF01279; Parathyroid; 1.  
DR PIRSF; PIRSF001832; PTH; 1.  
DR ProDom; PD010687; Pthyrdorm sub; 1.  
DR SMART; SM00087; PTH; 1.  
DR PROSITE; PS00335; PARATHYROID; 1.  
KW Hormone; Signal.  
FT SIGNAL 1 25 By similarity.  
FT PROPEP 26 31 By similarity.  
FT CHAIN 32 115 Parathyroid hormone.  
SQ SEQUENCE 115 AA; 12957 MW; FC38F77F1C8CFE56 CRC64;

Query Match 54.3%; Score 88; DB 1; Length 115;  
Best Local Similarity 67.7%; Pred. No. 0.0093;  
Matches 21; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 AVSIEIGGGGGGGGGLNSMERVWLRLKLDV 31  
:||||| :||||| :||||| :||||| :|||||  
DB 32 SVSEIQMHNLGKHLNSMERVWLRLKLDV 62

## RESULT 7

PTHY\_FELCA STANDARD; PRT; 115 AA.

PTHY\_PIG STANDARD; PRT; 115 AA.  
P01269;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Parathyroid hormone precursor (Parathyrin) (PTH).  
GN Name=PTH;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=87316938; PubMed=3628009;  
RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;  
RT "Nucleotide sequence of a full-length cDNA clone encoding  
preproparathyroid hormone from pig and rat."  
RL Nucleic Acids Res. 15:6740-6740(1987).  
RN [2]  
RP PROTEIN SEQUENCE OF 26-115.  
RX MEDLINE=76018954; PubMed=1164500;  
RA Chu L.I.H., Huang W.-Y., Littledike E.T., Hamilton J.W., Cohn D.V.;  
RT "Porcine preparathyroid hormone. Identification, biosynthesis, and  
partial amino acid sequence."  
RL Biochemistry 14:3631-3635(1975).  
RN [3]  
RP PROTEIN SEQUENCE OF 32-115.  
RX MEDLINE=74253311; PubMed=4840833;  
RA Sauer R.T., Nail H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,  
RA Potts J.T. Jr.;  
RT "The amino acid sequence of porcine parathyroid hormone."  
RL Biochemistry 13:1994-1999(1974).  
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in  
CC bone and preventing their renal excretion.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; X05722; CAA29193.1; -; mRNA.  
DR PIR; B26806; PTPG.  
DR HSP; P01270; 1BWX.  
DR InterPro; IPR001415; Parathyrd hrm.  
DR InterPro; IPR003625; Pthyrdorm sub.  
DR PANTHER; PTHR10541; Pthyrdorm sub; 1.  
DR Pfam; PF01279; Parathyroid; 1.  
DR PIRSF; PIRSF001832; PTH; 1.  
DR ProDom; PD010687; Pthyrdorm sub; 1.  
DR SMART; SM00087; PTH; 1.  
DR PROSITE; PS00335; PARATHYROID; 1.  
KW Direct protein sequencing; Hormone; Signal.  
FT SIGNAL 1 25  
FT PROPEP 26 31  
FT CHAIN 32 115 Parathyroid hormone.  
SQ SEQUENCE 115 AA; 12852 MW; 9FE8BCDE614BAC16 CRC64;

Query Match 51.9%; Score 84; DB 1; Length 115;  
Best Local Similarity 64.5%; Pred. No. 0.028;  
Matches 20; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 AVSIEIGGGGGGGGGLNSMERVWLRLKLDV 31  
:||||| :||||| :||||| :||||| :|||||  
DB 32 SVSEIQMHNLGKHLNSMERVWLRLKLDV 62

RESULT 8  
PTHY\_FELCA STANDARD; PRT; 115 AA.

```
AC Q9G67;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=PTH;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;
RT "Molecular cloning of feline preproparathyroid hormone.";
RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC bone and preventing their renal excretion (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF309967; AACG30545.1; -; mRNA.
DR HSSP; P01268; 12WC.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthythorm_sub.
DR PANTHER; PTHR10541; pthythorm_sub; 1.
DR Pfam; PF01279; Parathyroid; 1.
DR PIRSF; PIRSF001832; PTH; 1.
DR ProDom; PD010687; Pthythorm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
DR Hormone; Signal.
KW Hormone; Signal.
FT SIGNAL 1 25 By similarity.
FT PROPEP 26 31 By similarity.
FT CHAIN 32 115 Parathyroid hormone.
FT SEQUENCE 115 AA; 12921 MW; 80CD557CC6A1A47E CRC64;
SQ
Query Match 50.08; Score 81; DB 1; Length 115;
Best Local Similarity 61.3%; Pred. NO. 0.063;
Matches 19; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 AVSEIGGGGGGGGGLNSRVERVLRKQLQDV 31
DB 32 SVSEIQFMHNLGKHLSSRVERVLRKQLQDV 62
RESULT 9
Q80WZ2 RAT PRELIMINARY; PRT; 105 AA.
AC Q80WZ2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothalamic parathyroid hormone.
GN Name=PTH-(1-84);
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA STRAIN=Sprague-Dawley; TISSUE=Brain, Liver, and Parathyroid;
RX MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
RA Nukley M.T., Parimi S.A., Harvey S.;
RT "Sequence analysis of hypothalamic parathyroid hormone messenger
ribonucleic acid.";
RN [1]
RN NUCLEOTIDE SEQUENCE.
CC STRAIN=Sprague-Dawley; TISSUE=Brain, Liver, and Parathyroid;
RX MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
RA Nukley M.T., Parimi S.A., Harvey S.;
RT "Sequence analysis of hypothalamic parathyroid hormone messenger
ribonucleic acid.";
RT
```

```
RL Endocrinology 136:5600-5607(1995).
DR EMBL; S80127; AAP32220.1; -; mRNA.
DR HSSP; P01270; 12WB.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthythorm_sub.
DR PANTHER; PTHR10541; Pthythorm_sub; 1.
DR Pfam; PF01279; Parathyroid; 1.
DR PIRSF; PIRSF001832; PTH; 1.
DR ProDom; PD010687; Pthythorm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
SQ SEQUENCE 105 AA; 11684 MW; 18BE71B3F1CF5F70 CRC64;
Query Match 47.5%; Score 77; DB 2; Length 105;
Best Local Similarity 61.3%; Pred. NO. 0.17;
Matches 19; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
QY 1 AVSEIGGGGGGGGGLNSRVERVLRKQLQDV 31
DB 22 AVSEIQFMHNLGKHLSSRVERVLRKQLQDV 52
RESULT 10
PTHY_RAT
ID PTHY_RAT STANDARD; PRT; 115 AA.
AC P04089; Q63473;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=PTH;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=84135846; PubMed=6321505;
RA Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
RT "Gene encoding parathyroid hormone. Nucleotide sequence of the rat
gene and deduced amino acid sequence of rat preproparathyroid
hormone.";
RL J. Biol. Chem. 259:3320-3329(1984).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=87316938; PubMed=3628009;
RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT "Nucleotide sequence of a full-length cDNA clone encoding
preproparathyroid hormone from pig and rat.";
RL Nucleic Acids Res. 15:6740-6740(1987).
RN [3]
RN NUCLEOTIDE SEQUENCE OF 10-115.
RP TISSUE=Parathyroid;
RA Schmelzer H.-J., Gross G., Mayer H.;
RT "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
hormone.";
RL Adv. Gene Technol. 21:228-229(1984).
RN [4]
RN NUCLEOTIDE SEQUENCE OF 32-115.
RC STRAIN=Sprague-Dawley; TISSUE=Brain, Liver, and Parathyroid;
RX MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
RA Nukley M.T., Parimi S.A., Harvey S.;
RT "Sequence analysis of hypothalamic parathyroid hormone messenger
ribonucleic acid.";
RN [1]
RN NUCLEOTIDE SEQUENCE.
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
bone and preventing their renal excretion.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Hypothalamus and parathyroid gland.
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
```



RX MEDLINE=99455010; PubMed=10523642;  
RA Ito M., Yoshitaka K., Akechi M., Yamashita S., Takamatsu N.,  
RA Sugiyama K., Hibi M., Nakabeppu Y., Shiba T., Yamamoto K.-I.,  
RT "JSAPl, a novel jun N-terminal protein kinase (JNK)-binding protein  
RL that functions as a scaffold factor in the JNK signaling pathway."  
RL Mol. Cell. Biol. 19:7539-7548(1999).  
RN [3].  
RP NUCLEOTIDE SEQUENCE OF 660-1493.  
RC STRAIN=BAUB/C; TISSUE=Brain;  
RX MEDLINE=93227040; PubMed=8385802;  
RA Lange-Carter C.A., Pleiman C.M., Gardner A.M., Blumer K.J.,  
RA Johnson G.L.,  
RT "A divergence in the MAP kinase regulatory network defined by MEK  
RL kinase and Raf."  
RL Science 260:315-319(1993).  
RN [4].  
RP NUCLEOTIDE SEQUENCE OF 796-1493.  
RC STRAIN=BAUB/C; TISSUE=Heart;  
RA Whitmarsh A.J., Shore P., Sharrocks A.D., Davis R.J.,  
RN Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
RL [5].  
RP ENZYME REGULATION, AND MUTAGENESIS OF THR-1381 AND THR-1393.  
RX PubMed=9078260;  
RA Deak J.C., Templeton D.J.,  
RT "Regulation of the activity of MEK kinase 1 (MEKK1) by  
RL autophosphorylation within the kinase activation domain."  
RN Biochem. J. 322:185-192(1997).  
RN [6].  
RP FUNCTION, INTERACTIONS WITH IKKB AND MAP2K4, ENZYME REGULATION, AND  
RP MUTAGENESIS OF THR-1381; THR-1393; ISO-1394; PHE-1396; MET-1397;  
RP VAL-1401; LEU-1402; ARG-1403 AND GUY-1404.  
RX PubMed=14500727; DOI=10.1074/jbc.M304234200;  
RA Tu Z., Lee F.S.,  
RT "Subdomain VII is a specificity-determining region in MEKK1."  
RL J. Biol. Chem. 278:48498-48505(2003).  
CC -|- FUNCTION: Component of a protein kinase signal transduction  
CC cascade. Activates the ERK and JNK kinase pathways by  
CC phosphorylation of MAP2K1 and MAP2K4. Activates CHUK and IKKB,  
CC the central protein kinases of the NF-kappa-B pathway.  
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -|- COFACTOR: Magnesium.  
CC -|- ENZYME REGULATION: Activated by phosphorylation on Thr-1381 and  
CC Thr-1393.  
CC -|- SUBUNIT: Binds both upstream activators and downstream substrates  
CC in multimeric complexes through its N-terminus.  
CC -|- INTERACTION:  
CC O88351.Ikbbk; NBExp=1; IntAct=EBI-447913, EBI-447960;  
CC P47809.Map2k4; NBExp=1; IntAct=EBI-447913, EBI-447934;  
CC Q9QHG6.Sip1; NBExp=1; IntAct=EBI-447913, EBI-527020;  
CC -|- TISSUE SPECIFICITY: Highly expressed in the heart and spleen while  
CC a lower level expression is seen in the liver.  
CC -|- PTM: Autophosphorylated.  
CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP  
CC kinase kinase subfamily.  
CC -|- SIMILARITY: Contains 1 RING-type zinc finger.  
CC -|- SIMILARITY: Contains 1 SWIM-type zinc finger.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; AF117340; AAD25049.1; -; mRNA.  
CC EMBL; AB014614; BAA85878.1; -; mRNA.  
CC EMBL; L13103; AAA97500.1; ALT INIT; mRNA.  
CC EMBL; U23470; AAA85038.1; -; mRNA.  
CC HSSP; O16539; 1KVL.  
CC IntAct; P53349.  
CC Ensembl; ENSMUSG00000021754; Mus musculus.  
CC MGI; MGI:1346872; Map3k1.  
CC GO; GO:0001747; P:eye morphogenesis (sensu Mammalia); IMP.  
CC GO; GO:0030836; P:positive regulation of actin filament polym. . .; IMP.

DR GO; GO:0030334; P:regulation of cell migration; IMP.  
DR GO; GO:0007179; P:transforming growth factor beta receptor si. . .; IMP.  
DR GO; GO:0042060; P:wound healing; IMP.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR008271; Ser thr pkin AS.  
DR InterPro; IPR002290; Ser thr kinase.  
DR InterPro; IPR001903; UIM-  
DR InterPro; IPR001841; Znf RING.  
DR InterPro; IPR007527; Znf-SWIM.  
DR Pfam; PF04434; SWIM; 1.  
DR Pfam; PF02809; UIM; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00184; RING; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE; PS00089; ZF\_RING\_2; 1.  
DR PROSITE; PS0966; ZF-SWIM; 1.  
KW ATP-binding; Kinase; Magnesium; Metal-binding; Nucleotide-binding;  
KW Phosphorylation; Serine/threonine-protein kinase; Transferase; Zinc;  
KW Zinc-finger  
FT DOMAIN 1224 1489 Protein kinase.  
FT ZN\_FING 333 361 SWIM-type.  
FT ZN\_FING 438 487 RING-type.  
FT NP\_BIND 1230 1238 ATP (By similarity).  
FT COMPBIAS 25 32 Poly-Gly.  
FT COMPBIAS 74 149 Pro-rich.  
FT COMPBIAS 233 291 Pro-Ser.  
FT ACT\_SITE 1350 1350 Proton acceptor (By similarity).  
FT BINDING 1253 1253 ATP (By similarity).  
FT MOD\_RES 1381 1381 Phosphothreonine.  
FT MUTAGEN 1381 1381 T->A: Fails to activate MAP2K1, MAP2K4,  
FT MUTAGEN 1381 1381 MAP2K7, CHUK and IKKB.  
FT MUTAGEN 1381 1381 T->E: Loss of kinase activity and  
FT MUTAGEN 1381 1381 autophosphorylation.  
FT MUTAGEN 1381 1381 T->S: Reduced kinase activity and  
FT MUTAGEN 1381 1381 autophosphorylation.  
FT MUTAGEN 1381 1381 T->A: Loss of kinase activity and  
FT MUTAGEN 1381 1381 autophosphorylation. Fails to activate  
FT MUTAGEN 1381 1381 MAP2K1, MAP2K4, MAP2K7, CHUK and IKKB.  
FT MUTAGEN 1381 1381 T->E: Loss of kinase activity and  
FT MUTAGEN 1381 1381 autophosphorylation.  
FT MUTAGEN 1381 1381 T->S: Reduced kinase activity and  
FT MUTAGEN 1381 1381 autophosphorylation.  
FT MUTAGEN 1381 1381 I->A: Loss of NF-kappa-B transcription  
FT MUTAGEN 1381 1381 factor activity and reduced ability to  
FT MUTAGEN 1381 1381 activate MAP2K1, MAP2K4, MAP2K7. No  
FT MUTAGEN 1381 1381 effect on AP-1 activity or activation of  
FT MUTAGEN 1381 1381 CHUK and IKKB. Loss of binding to IKKB.  
FT MUTAGEN 1381 1381 F->A: Loss of AP-1 and NF-kappa-B  
FT MUTAGEN 1381 1381 transcription factor activity. Reduced  
FT MUTAGEN 1381 1381 ability to activate MAP2K1, MAP2K4,  
FT MUTAGEN 1381 1381 MAP2K7, CHUK and IKKB.  
FT MUTAGEN 1381 1381 V->A: Loss of AP-1 and NF-kappa-B  
FT MUTAGEN 1381 1381 transcription factor activity. Reduced  
FT MUTAGEN 1381 1381 ability to activate MAP2K1, MAP2K4,  
FT MUTAGEN 1381 1381 MAP2K7, CHUK and IKKB.  
FT MUTAGEN 1381 1381 L->A: Loss of AP-1 transcription factor  
FT MUTAGEN 1381 1381 activity and reduced ability to activate  
FT MUTAGEN 1381 1381 CHUK and IKKB. No effect on NF-kappa-B  
FT MUTAGEN 1381 1381 activity or activation of MAP2K1, MAP2K4,  
FT MUTAGEN 1381 1381 MAP2K7. Loss of binding to MAP2K4.  
FT MUTAGEN 1381 1381 R->A: Loss of AP-1 transcription factor  
FT MUTAGEN 1381 1381 activity, no effect on NF-kappa-B



```

FT MUTAGEN 1404 1404 activity.
FT G->A; Loss of AP-1 and NF-kappa-B
FT transcription factor activity.
FT GGGALGGGA -> ALQSG (in Ref. 2).
FT Missing (in Ref. 2).
FT V -> E (in Ref. 2).
FT CONFLICT 30 39
FT CONFLICT 103 103
FT CONFLICT 257 257
FT CONFLICT 307 307
FT CONFLICT 413 413
FT CONFLICT 559 559
FT CONFLICT 883 883
FT CONFLICT 1467 1467
FT V -> L (in Ref. 3).
SQ SEQUENCE 1493 AA; 161289 MW; CA65C9B7703C6BF9 CRC64;

Query Match 45.4%; Score 73.5; DB 1; Length 1493;
Best Local Similarity 34.0%; Pred. No. 6.8; Indels 19; Gaps 1;
Matches 17; Conservative 4; Mismatches 10;

QY 1 AVSEITGGGGGGGGLN-----SMERVEWRKKLQDV 31
DB 20 ASPEAGGGGGGALQSGCAPAAGALLRPGSAGRERADWRRLQAKV 69

RESULT 13
Q6K708 ORYSA
ID Q6K708 ORYSA PRELIMINARY; PRT; 770 AA.
AC Q6K708;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative ethylene receptor-like protein 2.
CN Name=P0474P11.19-1; Synonyms=QJ1119.A01.4-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
[2]
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RA "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC
RT clone:Oull119.A01.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004878; BAD23111.1; -; Genomic DNA.
DR EMBL; AP004020; BAD22879.1; -; Genomic DNA.
DR Gramene; Q6K708; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR003661; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; HsKA; 1.
DR Pfam; PF00072; Response_reg; 1.
DR Pfam; PF00072; Response_reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00388; HsKA; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
KW Receptor.
SQ SEQUENCE 836 AA; 92644 MW; 324D3E7F0B97A85A CRC64;

Query Match 43.5%; Score 70.5; DB 2; Length 836;
Best Local Similarity 55.6%; Pred. No. 8.5; Indels 3; Gaps 2;
Matches 15; Conservative 5; Mismatches 4;

QY 6 GGGGGGGGGLNSMERV-EWLRKKLQDV 31
DB 112 GGGGGGGGGLNSMERV-EWLRKKLQDV 136

RESULT 15

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Search completed: November 21, 2005, 16:15:13  
Job time : 148.5 secs

Search completed: November 21, 2005, 16:15:13  
Job time : 148.5 secs

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OM protein - protein search, using sw model

Run On: November 21, 2005, 16:05:03 ; Search time 33 Seconds  
(without alignments)  
77.665 Million cell updates/sec

Title: US-09-475-158A-5  
Perfect score: 162  
Sequence: 1 AVSEITGGGGGGGLNSMERVELRKLQDV 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	100	61.7	38	4	PCT-US95-15800-29
2	98	60.5	35	1	US-08-142-551B-34
3	98	60.5	35	1	US-08-142-551B-37
4	98	60.5	35	1	US-08-142-551B-46
5	96	59.3	35	1	US-08-142-551B-40
6	96	59.3	35	1	US-08-142-551B-52
7	96	59.3	35	1	US-08-142-551B-56
8	95	58.6	33	2	US-09-447-800-6
9	95	58.6	34	2	US-09-447-800-5
10	94	58.0	34	2	US-09-044-536A-12
11	94	58.0	34	2	US-09-843-221A-17
12	94	58.0	34	2	US-09-843-221A-18
13	94	58.0	34	2	US-09-843-221A-162
14	94	58.0	34	2	US-09-843-221A-163
15	94	58.0	35	1	US-08-142-551B-43
16	93	57.4	34	2	US-09-044-536A-8
17	92	56.8	31	1	US-08-262-495C-3
18	92	56.8	31	1	US-08-691-647C-1
19	92	56.8	31	1	US-08-691-647C-6
20	92	56.8	31	2	US-08-904-760B-1
21	92	56.8	31	2	US-08-904-760B-6
22	92	56.8	31	2	US-08-904-760B-14
23	92	56.8	31	2	US-08-904-760B-32
24	92	56.8	31	2	US-09-406-813-2
25	92	56.8	31	2	US-09-536-785A-1
26	92	56.8	31	2	US-09-536-785A-6
27	92	56.8	31	2	US-09-536-785A-14

28	92	56.8	31	2	US-09-536-785A-32	Sequence 32, Appl
29	92	56.8	31	2	US-09-843-221A-27	Sequence 27, Appl
30	92	56.8	31	2	US-09-843-221A-165	Sequence 165, App
31	92	56.8	31	2	US-09-623-548A-271	Sequence 271, App
32	92	56.8	31	2	US-09-657-276-271	Sequence 271, App
33	92	56.8	33	2	US-09-447-800-9	Sequence 9, Appli
34	92	56.8	34	1	US-07-765-373-1	Sequence 1, Appli
35	92	56.8	34	1	US-08-033-099-1	Sequence 1, Appli
36	92	56.8	34	1	US-08-262-495C-1	Sequence 1, Appli
37	92	56.8	34	1	US-07-915-247A-1	Sequence 1, Appli
38	92	56.8	34	1	US-08-443-863-1	Sequence 1, Appli
39	92	56.8	34	1	US-08-448-070-1	Sequence 1, Appli
40	92	56.8	34	1	US-08-488-105-7	Sequence 7, Appli
41	92	56.8	34	1	US-08-468-275-6	Sequence 6, Appli
42	92	56.8	34	1	US-08-449-500-1	Sequence 1, Appli
43	92	56.8	34	1	US-08-449-317A-1	Sequence 1, Appli
44	92	56.8	34	1	US-08-142-551B-2	Sequence 2, Appli
45	92	56.8	34	1	US-08-477-022-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
PCT-US95-15800-29  
; Sequence 29, Application PC/TUS9515800  
; GENERAL INFORMATION:  
; APPLICANT: BioNebraska, Inc.  
; TITLE OF INVENTION: PRODUCTION OF PEPTIDES USING  
; RECOMBINANT FUSION PROTEIN CONSTRUCTS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 Norwest Center, 90 S. 7th Street  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: U.S.A.  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/15800  
; FILING DATE: 07-DEC-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/350,530  
; FILING DATE: 07-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 8648.45USWO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/332-5300  
; TELEFAX: 612/332-9081  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 38 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; PCT-US95-15800-29  
Query Match 61.7%; Score 100; DB 4; Length 38;  
Best Local Similarity 74.2%; Pred. No. 1.8e-05;

US-08-142-35B-48  
; Sequence 46, Application US/0814235B-48  
; Patent No. 5814603  
; GENERAL INFORMATION:  
; APPLICANT: Oldenburg, Kevin R  
; APPLICANT: Selick, Harold E.

```
;
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
;
; US-08-142-551B-46
;
; Query Match 60.5%; Score 98; DB 1; Length 35;
; Best Local Similarity 71.0%; Pred. No. 2.8e-05;
; Matches 22; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
;
; Qy 1 AVSEIGGGGGGGGGLNSMERVWLKQLQDV 31
; :||| :|||:|||||
; Db 1 SVSEIQLHNGKHLNSLSEVWLKQLQDV 31
;
; RESULT 5
; US-08-142-551B-40
; Sequence 40, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
```

```
;
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
;
; US-08-142-551B-40
;
; Query Match 59.3%; Score 96; DB 1; Length 35;
; Best Local Similarity 71.0%; Pred. No. 4.9e-05;
; Matches 22; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
;
; Qy 1 AVSEIGGGGGGGGGLNSMERVWLKQLQDV 31
; :||| :|||:|||||
; Db 1 SVSEIQLHNGKHLNSLSEVWLKQLQDV 31
;
; RESULT 6
; US-08-142-551B-52
; Sequence 52, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 35 amino acids
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
;
US-08-142-551B-52
Query Match 59.3%; Score 96; DB 1; Length 35;
Best Local Similarity 71.0%; Pred. No. 4.9e-05;
Matches 22; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 AVSEIGGGGGGGGGLNSMERVWLKKLDV 31
Db 1 SVSEIQLLHNLGGLNSLSEVWLKKLDV 31

RESULT 7
US-08-142-551B-56
; Sequence 56, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
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;
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 14-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 35 amino acids
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
;
US-08-142-551B-56
Query Match 59.3%; Score 96; DB 1; Length 35;
Best Local Similarity 71.0%; Pred. No. 4.9e-05;
Matches 22; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 AVSEIGGGGGGGGGLNSMERVWLKKLDV 31
Db 1 SVSEIQLLHNLGGLNSLSEVWLKKLDV 31

RESULT 8
US-09-447-800-6
; Sequence 6, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, P. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
;
US-09-447-800-6
Query Match 58.6%; Score 95; DB 2; Length 33;
Best Local Similarity 74.2%; Pred. No. 6.1e-05;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AVSEIGGGGGGGGGLNSMERVWLKKLDV 31
Db 1 AVSEIQLMHNLGKHLNSMERVWLKKLDV 31
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```
RESULT 9
US-09-447-800-5
; Sequence 5, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-09-447-800-5

Query Match      58.6%; Score 95; DB 2; Length 34;
Best Local Similarity 74.2%; Pred. No. 6.3e-05;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 1 AVSEITGGGGGGGGLNSMERVEWLRLKQLQDV 31
    ||||| | ||||| ||||| |||||
Db 1 AVSEITQLMHNGLKHLNSMERVEWLRLKQLQDV 31

RESULT 10
US-09-044-536A-12
; Sequence 12, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
```

```
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /product= "Xaa=Ala(2-Naph)"
US-09-044-536A-12

Query Match      58.0%; Score 94; DB 2; Length 34;
Best Local Similarity 71.0%; Pred. No. 8.3e-05;
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Oy 1 AVSEITGGGGGGGGLNSMERVEWLRLKQLQDV 31
    ||||| | ||||| ||||| |||||
Db 1 SVSEITQLMHNDRGKHLNSMERVEWLRLKQLQDV 31

RESULT 11
US-09-843-221A-17
; Sequence 17, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 17
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-17

Query Match      58.0%; Score 94; DB 2; Length 34;
Best Local Similarity 71.0%; Pred. No. 8.3e-05;
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Oy 1 AVSEITGGGGGGGGLNSMERVEWLRLKQLQDV 31
    ||||| | ||||| ||||| |||||
Db 1 SVSEITQLMHNDRGKHLNSMERVEWLRLKQLQDV 31

RESULT 12
US-09-843-221A-18
; Sequence 18, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: RELATED PROTEIN
```

```
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; TYPE: PRT
; LENGTH: 34
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-18

Query Match      58.0%; Score 94; DB 2; Length 34;
Best Local Similarity 71.0%; Pred. No. 8.3e-05;
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      1 AVSEIGGGGGGGGLNSMERVWLKRLQDV 31
       :||||| | ||||| ||||| |||||
Db      1 SVSEIQLMHNKGLNSMERVWLKRLQDV 31

RESULT 13
US-09-843-221A-162
; Sequence 162, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
; TYPE: PRT
; LENGTH: 34
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-162

Query Match      58.0%; Score 94; DB 2; Length 34;
Best Local Similarity 71.0%; Pred. No. 8.3e-05;
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      1 AVSEIGGGGGGGGLNSMERVWLKRLQDV 31
       :||||| | ||||| ||||| |||||
Db      1 SVSEIQLMHNKGLNSMERVWLKRLQDV 31

RESULT 14
US-09-843-221A-163
; Sequence 163, Application US/09843221A
; Patent No. 6756480
```

```
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-163

Query Match      58.0%; Score 94; DB 2; Length 34;
Best Local Similarity 71.0%; Pred. No. 8.3e-05;
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      1 AVSEIGGGGGGGGLNSMERVWLKRLQDV 31
       :||||| | ||||| ||||| |||||
Db      1 SVSEIQLMHNKGLNSMERVWLKRLQDV 31

RESULT 15
US-08-142-551B-43
; Sequence 43, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
```



```

; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note="Where "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
;
US-08-142-551B-43

Query Match      58.0%; Score 94; DB 1; Length 35;
Best Local Similarity 71.0%; Pred. No. 8.6e-05;
Matches 22; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy      1 AVSEIGGGGGGGGINSMERVELRKKLQDV 31
       :|||||:|:|||||:|||||:|||||
Db      1 SVSEIQLLHGLGKHLNSLSEVELRKKLQDV 31

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Search completed: November 21, 2005, 16:16:22  
Job time : 34 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 16:15:23 ; Search time 110.5 Seconds  
(without alignments)  
117.219 Million cell updates/sec

Title: US-09-475-158A-5  
Perfect score: 162  
Sequence: 1 AVSEIGGGGGGGGLNSMERVWLKRLQDV 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	64.2	89	5	US-10-997-078-132
2	103	63.6	91	5	US-10-997-762-19
3	103	63.6	91	5	US-10-997-822-4
4	103	63.6	141	5	US-10-997-762-21
5	95	58.6	33	4	US-10-361-928-6
6	95	58.6	34	4	US-10-361-928-5
7	94	58.0	31	5	US-10-892-025-20
8	94	58.0	34	3	US-09-843-221A-17
9	94	58.0	34	3	US-09-843-221A-18
10	94	58.0	34	3	US-09-843-221A-162
11	94	58.0	34	3	US-09-843-221A-163
12	94	58.0	34	3	US-09-999-608-17
13	94	58.0	34	3	US-09-999-608-18
14	94	58.0	34	3	US-09-999-608-162
15	94	58.0	34	3	US-09-999-608-163
16	94	58.0	34	4	US-10-839-037-17
17	94	58.0	34	4	US-10-839-037-18
18	94	58.0	34	4	US-10-839-037-162
19	94	58.0	34	4	US-10-839-037-163
20	93	57.4	31	5	US-10-892-025-21
21	93	57.4	31	5	US-10-892-025-22
22	92	56.8	31	3	US-09-169-786-2
23	92	56.8	31	3	US-09-843-221A-27
24	92	56.8	31	3	US-09-843-221A-165
25	92	56.8	31	3	US-09-999-608-27
26	92	56.8	31	3	US-09-999-608-165
27	92	56.8	31	4	US-10-440-473-2

28	92	56.8	31	4	US-10-839-037-27
29	92	56.8	31	4	US-10-839-037-165
30	92	56.8	31	5	US-10-892-025-1
31	92	56.8	31	6	US-11-066-697-271
32	92	56.8	31	6	US-11-040-557-2
33	92	56.8	32	5	US-10-892-025-2
34	92	56.8	32	6	US-11-040-557-20
35	92	56.8	33	4	US-10-361-928-9
36	92	56.8	33	5	US-10-892-025-3
37	92	56.8	33	6	US-11-040-557-1
38	92	56.8	33	6	US-11-040-557-21
39	92	56.8	34	3	US-09-169-786-3
40	92	56.8	34	3	US-09-858-880-5
41	92	56.8	34	3	US-09-928-047B-6
42	92	56.8	34	3	US-09-843-221A-16
43	92	56.8	34	3	US-09-843-221A-161
44	92	56.8	34	3	US-09-928-048A-6
45	92	56.8	34	3	US-09-999-608-16

## ALIGNMENTS

### RESULT 1

US-10-997-078-132  
; Sequence 132, Application US/10997078  
; Publication No. US2005022144A1  
; GENERAL INFORMATION:  
; APPLICANT: Wagner, F.  
; APPLICANT: Peng, L.  
; APPLICANT: Xia, U.  
; APPLICANT: Holmquist, B.  
; APPLICANT: Restoragen, Inc.  
; TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptide  
; FILE REFERENCE: 1627.010US1  
; CURRENT APPLICATION NUMBER: US/10/997,078  
; CURRENT FILING DATE: 2004-11-24  
; PRIOR APPLICATION NUMBER: PCT/US03/16643  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US 60/383,370  
; PRIOR FILING DATE: 2002-05-24  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 132  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: A synthetic sequence for the T7tagVg-PTH(1-34) cassette.  
US-10-997-078-132

Query Match 64.2% ; Score 104; DB 5; Length 89;  
Best Local Similarity 59.0% ; Pred. No. 6.7e-05;  
Matches 23; Conservative 1; Mismatches 1; Indels 12; Gaps 1;

QY 5 IGGGGGG-----GGGLNSMERVWLKRLQDV 31  
:|||||  
DB 48 VGGGGGPRSVSEIQLMHNGLHLSMERVWLKRLQDV 86

### RESULT 2

US-10-997-762-19  
; Sequence 19, Application US/10997762  
; Publication No. US2005022731A1  
; GENERAL INFORMATION:  
; APPLICANT: Seo, Jin Seog  
; APPLICANT: Strydom, Daniel  
; APPLICANT: Holmquist, Barton  
; APPLICANT: Restoragen, Inc.  
; TITLE OF INVENTION: Polypeptide Cleavage Process  
; FILE REFERENCE: 1627.026US1  
; CURRENT APPLICATION NUMBER: US/10/997,762  
; CURRENT FILING DATE: 2004-11-24

; PRIOR APPLICATION NUMBER: PCT/US03/16468  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US 60/383,488  
; PRIOR FILING DATE: 2002-05-24  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 91  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: A synthetic chimeric protein  
US-10-997-762-19

Query Match 63.6%; Score 103; DB 5; Length 91;  
Best Local Similarity 56.1%; Pred. No. 9e-05; 3; Indels 14; Gaps 1;  
Matches 23; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 5 IGGGGGG-----GGGLNSMERVEWLKKLDV 31  
:|||||  
DB 48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLKKLDV 88

## RESULT 3

US-10-997-822-4  
; Sequence 4, Application US/10997822  
; Publication No. US20050227314A1  
; GENERAL INFORMATION:  
; APPLICANT: Holmquist, B.  
; APPLICANT: Strydom, D.  
; APPLICANT: Gensalk, X.  
; APPLICANT: Cryer, R.  
; TITLE OF INVENTION: POLYPEPTIDE CLEAVAGE PROCESS  
; FILE REFERENCE: 1627.011US1  
; CURRENT APPLICATION NUMBER: US/10/997,822  
; CURRENT FILING DATE: 2004-11-24  
; PRIOR APPLICATION NUMBER: PCT/US03/16647  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US 60/383,484  
; PRIOR FILING DATE: 2002-05-24  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 91  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of a synthetic chimeric protein.  
US-10-997-822-4

Query Match 63.6%; Score 103; DB 5; Length 91;  
Best Local Similarity 56.1%; Pred. No. 9e-05; 3; Indels 14; Gaps 1;  
Matches 23; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 5 IGGGGGG-----GGGLNSMERVEWLKKLDV 31  
:|||||  
DB 48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLKKLDV 88

## RESULT 4

US-10-997-762-21  
; Sequence 21, Application US/10997762  
; Publication No. US20050227313A1  
; GENERAL INFORMATION:  
; APPLICANT: Seo, Jin Seog  
; APPLICANT: Strydom, Daniel  
; APPLICANT: Holmquist, Barton  
; APPLICANT: Restoragen Inc.  
; TITLE OF INVENTION: Polypeptide Cleavage Process  
; FILE REFERENCE: 1627.026US1  
; CURRENT APPLICATION NUMBER: US/10/997,762  
; CURRENT FILING DATE: 2004-11-24  
; PRIOR APPLICATION NUMBER: PCT/US03/16468

; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US 60/383,488  
; PRIOR FILING DATE: 2002-05-24  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 141  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: A synthetic chimeric protein  
US-10-997-762-21

Query Match 63.6%; Score 103; DB 5; Length 141;  
Best Local Similarity 56.1%; Pred. No. 0.00014;  
Matches 23; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 5 IGGGGGG-----CGGLNSMERVEWLKKLDV 31  
:|||||  
DB 48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLKKLDV 88

## RESULT 5

US-10-361-928-6  
; Sequence 6, Application US/10361928  
; Publication No. US20030144209A1  
; GENERAL INFORMATION:  
; APPLICANT: BRINGHURST, F. RICHARD  
; APPLICANT: TAKASU, HISASHI  
; APPLICANT: GARDELLA, THOMAS J.  
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)  
; FILE REFERENCE: 0609.4630002  
; CURRENT APPLICATION NUMBER: US/10/361,928  
; CURRENT FILING DATE: 2003-02-11  
; PRIOR APPLICATION NUMBER: 09/447,800  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: 60/110,152  
; PRIOR FILING DATE: 1998-11-25  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Desamino Ala  
US-10-361-928-6

Query Match 58.6%; Score 95; DB 4; Length 33;  
Best Local Similarity 74.2%; Pred. No. 0.00031;  
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AVSEIGGGGGGGGLNSMERVEWLKKLDV 31  
:|||||  
DB 1 AVSEIQLMHNLGKHLNSMERVEWLKKLDV 31

## RESULT 6

US-10-361-928-5  
; Sequence 5, Application US/10361928  
; Publication No. US20030144209A1  
; GENERAL INFORMATION:  
; APPLICANT: BRINGHURST, F. RICHARD  
; APPLICANT: TAKASU, HISASHI  
; APPLICANT: GARDELLA, THOMAS J.  
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)  
; FILE REFERENCE: 0609.4630002  
; CURRENT APPLICATION NUMBER: US/10/361,928  
; CURRENT FILING DATE: 2003-02-11

;; PRIOR APPLICATION NUMBER: 09/447,800  
;; PRIOR FILING DATE: 1999-11-23  
;; PRIOR APPLICATION NUMBER: 60/110,152  
;; PRIOR FILING DATE: 1998-11-25  
;; NUMBER OF SEQ ID NOS: 10  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 5  
;; LENGTH: 34  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: MOD\_RES  
;; LOCATION: (1)  
;; OTHER INFORMATION: Desamino Ala  
US-10-361-928-5

Query Match 58.6%; Score 95; DB 4; Length 34;  
Best Local Similarity 74.2%; Pred. No. 0.00032;  
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Qy 1 AVSEIGGGGGGGGGLNSMERVWLKQLQDV 31  
Db 1 AVSEIQLMHNLGKHLNSMERVWLKQLQDV 31

## RESULT 7

US-10-892-025-20  
;; Sequence 20, Application US/10892025  
;; Publication No. US20050065071A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Morley, Paul  
;; TITLE OF INVENTION: CYCLIC ANALOGS OF HUMAN PARATHYROID  
;; TITLE OF INVENTION: HORMONE FOR THE TREATMENT OF CONDITIONS CHARACTERIZED BY  
;; TITLE OF INVENTION: HYPERPROLIFERATIVE SKIN CELLS  
;; FILE REFERENCE: 3583.1000-001  
;; CURRENT APPLICATION NUMBER: US/10/892,025  
;; CURRENT FILING DATE: 2004-07-15  
;; PRIOR APPLICATION NUMBER: 60/487,513  
;; PRIOR FILING DATE: 2003-07-15  
;; NUMBER OF SEQ ID NOS: 42  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 20  
;; LENGTH: 31  
;; TYPE: PRT  
;; ORGANISM: Homo sapien  
;; FEATURE:  
;; NAME/KEY: SITE  
;; LOCATION: 1  
;; OTHER INFORMATION: NHR; wherein R is hydrogen or a linear or branched  
;; OTHER INFORMATION: chain alkyl, acyl or aryl group  
;; FEATURE:  
;; NAME/KEY: VARIANT  
;; LOCATION: 8  
;; OTHER INFORMATION: is selected from the group consisting of Met,  
;; OTHER INFORMATION: norisoleucine, and a hydrophobic amino acid  
;; FEATURE:  
;; NAME/KEY: SITE  
;; LOCATION: 31  
;; OTHER INFORMATION: Y; where Y is X, His-X, His-Asn-X, or  
;; OTHER INFORMATION: His-Asn-Phe-X; where X is OR or NHR; and R is  
;; OTHER INFORMATION: hydrogen or a linear or branched chain alkyl, acyl  
;; OTHER INFORMATION: or aryl group  
US-10-892-025-20

Query Match 58.0%; Score 94; DB 5; Length 31;  
Best Local Similarity 71.0%; Pred. No. 0.00039;  
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
Qy 1 AVSEIGGGGGGGGGLNSMERVWLKQLQDV 31  
Db 1 SVSEIQLMHNLGKHLNSMERVWLKQLQDV 31

## RESULT 8

US-09-843-221A-17  
;; Sequence 17, Application US/09843221A  
;; Publication No. US20030039654A1  
;; GENERAL INFORMATION:  
;; APPLICANT: KOSTENUIK, PAUL  
;; APPLICANT: LIU, CHUAN-FA  
;; APPLICANT: LACEY, DAVID LEE  
;; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
;; TITLE OF INVENTION: RELATED PROTEIN  
;; FILE REFERENCE: A-665B  
;; CURRENT APPLICATION NUMBER: US/09/843,221A  
;; CURRENT FILING DATE: 2001-04-26  
;; PRIOR APPLICATION NUMBER: 60/266,673  
;; PRIOR FILING DATE: 2001-02-06  
;; PRIOR APPLICATION NUMBER: 60/214,860  
;; PRIOR FILING DATE: 2000-06-28  
;; PRIOR APPLICATION NUMBER: 60/200,053  
;; PRIOR FILING DATE: 2000-04-27  
;; NUMBER OF SEQ ID NOS: 170  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 17  
;; LENGTH: 34  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: modified human PTH  
US-09-843-221A-17

Query Match 58.0%; Score 94; DB 3; Length 34;  
Best Local Similarity 71.0%; Pred. No. 0.00042;  
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
Qy 1 AVSEIGGGGGGGGGLNSMERVWLKQLQDV 31  
Db 1 SVSEIQLMHNLRGKHLNSMERVWLKQLQDV 31

## RESULT 9

US-09-843-221A-18  
;; Sequence 18, Application US/09843221A  
;; Publication No. US20030039654A1  
;; GENERAL INFORMATION:  
;; APPLICANT: KOSTENUIK, PAUL  
;; APPLICANT: LIU, CHUAN-FA  
;; APPLICANT: LACEY, DAVID LEE  
;; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
;; TITLE OF INVENTION: RELATED PROTEIN  
;; FILE REFERENCE: A-665B  
;; CURRENT APPLICATION NUMBER: US/09/843,221A  
;; CURRENT FILING DATE: 2001-04-26  
;; PRIOR APPLICATION NUMBER: 60/266,673  
;; PRIOR FILING DATE: 2001-02-06  
;; PRIOR APPLICATION NUMBER: 60/214,860  
;; PRIOR FILING DATE: 2000-06-28  
;; PRIOR APPLICATION NUMBER: 60/200,053  
;; PRIOR FILING DATE: 2000-04-27  
;; NUMBER OF SEQ ID NOS: 170  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 18  
;; LENGTH: 34  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: modified human PTH  
US-09-843-221A-18

Query Match 58.0%; Score 94; DB 3; Length 34;  
Best Local Similarity 71.0%; Pred. No. 0.00042;  
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
Qy 1 AVSEIGGGGGGGGGLNSMERVWLKQLQDV 31

```

; LOCATION: (34).....(34)
; OTHER INFORMATION: Optional linker and Pc domain attached at the C-terminus
US-09-843-221A-163

Query Match      58.0%; Score 94; DB 3; Length 34;
Best Local Similarity 71.0%; Pred. No. 0.00042;
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGLNSMERVWLKRLQDV 31
   :||||| | ||||| ||||| |||||
Db 1 SVSEIQLMHNKGLNSMERVWLKRLQDV 31

RESULT 12
US-09-999-608-17
; Sequence 18, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: GEGG, COLIN V.
; APPLICANT: JAROSINSKI, MARK ANTHONY
; APPLICANT: KINSTLER, OLAF BORIS
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
; TITLE OF INVENTION: HORMONE-RELATED PROTEIN
; FILE REFERENCE: A-665C
; CURRENT APPLICATION NUMBER: US/09/999,608
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/843,221
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-999-608-17

Query Match      58.0%; Score 94; DB 3; Length 34;
Best Local Similarity 71.0%; Pred. No. 0.00042;
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGLNSMERVWLKRLQDV 31
   :||||| | ||||| ||||| |||||
Db 1 SVSEIQLMHNKGLNSMERVWLKRLQDV 31

RESULT 13
US-09-999-608-18
; Sequence 18, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: GEGG, COLIN V.
; APPLICANT: JAROSINSKI, MARK ANTHONY
; APPLICANT: KINSTLER, OLAF BORIS
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
; TITLE OF INVENTION: HORMONE-RELATED PROTEIN
; FILE REFERENCE: A-665C
; CURRENT APPLICATION NUMBER: US/09/999,608
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/843,221
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/214,860
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Preferred embodiments - PTH
US-09-843-221A-162

Query Match      58.0%; Score 94; DB 3; Length 34;
Best Local Similarity 71.0%; Pred. No. 0.00042;
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGLNSMERVWLKRLQDV 31
   :||||| | ||||| ||||| |||||
Db 1 SVSEIQLMHNKGLNSMERVWLKRLQDV 31

RESULT 11
US-09-843-221A-163
; Sequence 163, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Preferred embodiments - PTH
US-09-843-221A-162

Query Match      58.0%; Score 94; DB 3; Length 34;
Best Local Similarity 71.0%; Pred. No. 0.00042;
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGLNSMERVWLKRLQDV 31
   :||||| | ||||| ||||| |||||
Db 1 SVSEIQLMHNKGLNSMERVWLKRLQDV 31

RESULT 11
US-09-843-221A-163
; Sequence 163, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Preferred embodiments - PTH
US-09-843-221A-162

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; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: US 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 193  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: modified human PTH  
US-09-999-608-18

Query Match 58.0%; Score 94; DB 3; Length 34;  
Best Local Similarity 71.0%; Pred. No. 0.00042;  
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31  
:||||| - |||||||  
Db 1 SVSEIQLMHNKKGKHLNSMERVEWLRKKLQDV 31

## RESULT 14

US-09-999-608-162  
; Sequence 162, Application US/09999608  
; Publication No. US20050124537A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENUK, PAUL  
; APPLICANT: GEGG, COLIN V.  
; APPLICANT: JAROSINSKI, MARK ANTHONY  
; APPLICANT: KINSTLER, OLAF BORIS  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID  
; TITLE OF INVENTION: HORMONE-RELATED PROTEIN  
; FILE REFERENCE: A-665C  
; CURRENT APPLICATION NUMBER: US/09/999,608  
; CURRENT FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 09/843,221  
; PRIOR FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: US 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: US 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: US 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 193  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 162  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Preferred embodiments - PTH

; NAME/KEY: misc feature  
; LOCATION: (34)..(34)  
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus  
US-09-999-608-162

Query Match 58.0%; Score 94; DB 3; Length 34;  
Best Local Similarity 71.0%; Pred. No. 0.00042;  
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31  
:||||| - |||||||  
Db 1 SVSEIQLMHNKKGKHLNSMERVEWLRKKLQDV 31

## RESULT 15

US-09-999-608-163  
; Sequence 163, Application US/09999608  
; Publication No. US20050124537A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENUK, PAUL

; APPLICANT: GEGG, COLIN V.  
; APPLICANT: JAROSINSKI, MARK ANTHONY  
; APPLICANT: KINSTLER, OLAF BORIS  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID  
; TITLE OF INVENTION: HORMONE-RELATED PROTEIN  
; FILE REFERENCE: A-665C  
; CURRENT APPLICATION NUMBER: US/09/999,608  
; CURRENT FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 09/843,221  
; PRIOR FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: US 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: US 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: US 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 193  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 163  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Preferred embodiments - PTH  
; NAME/KEY: misc feature  
; LOCATION: (34)..(34)  
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus  
US-09-999-608-163

Query Match 58.0%; Score 94; DB 3; Length 34;  
Best Local Similarity 71.0%; Pred. No. 0.00042;  
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31  
:||||| - |||||||  
Db 1 SVSEIQLMHNKKGKHLNSMERVEWLRKKLQDV 31

Search completed: November 21, 2005, 16:34:42  
Job time : 110.5 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 16:16:29 ; Search time 4 Seconds  
(without alignments)

8.756 Million cell updates/sec

Title: US-09-475-158a-5

Perfect score: 162

Sequence: 1 AVSEIGGGGGGGGGLNEMERVEWLKKLQDV 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:\*

- 1: /cgn2\_6/ptodata/2/pubaa/US10 NEW PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubaa/US06 NEW PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubaa/US07 NEW PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubaa/US08 NEW PUB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubaa/US09 NEW PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubaa/PCT NEW PUB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubaa/US11 NEW PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubaa/US60 NEW PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68.5	42.3	1493	7	US-11-004-057-4
2	60	37.0	579	1	US-10-975-798-4
3	60	37.0	580	1	US-10-975-798-3
4	56.5	34.9	1493	7	US-11-004-057-21
5	54	33.3	157	1	US-10-957-569-64
6	54	33.3	200	1	US-10-841-129-7
7	54	33.3	200	7	US-11-060-659-32
8	54	33.3	269	1	US-10-131-826A-532
9	54	33.3	562	7	US-11-065-943-20
10	54	33.3	562	7	US-11-065-943-22
11	54	33.3	562	7	US-11-065-943-24
12	54	33.3	562	7	US-11-065-943-26
13	54	33.3	562	7	US-11-065-943-28
14	54	33.3	562	7	US-11-065-943-30
15	54	33.3	562	7	US-11-065-943-32
16	54	33.3	562	7	US-11-065-943-34
17	54	33.3	562	7	US-11-065-943-36
18	54	33.3	562	7	US-11-065-943-38
19	51	31.5	327	1	US-10-512-184-64
20	51	31.5	1127	7	US-11-077-550-40
21	51	31.5	1127	7	US-11-077-550-50
22	51	31.5	1127	7	US-11-077-550-54
23	51	31.5	1127	7	US-11-077-550-58
24	51	31.5	1130	7	US-11-077-550-44
25	49	30.2	888	1	US-10-131-826A-544

26	48	29.6	10	1	US-10-512-184-44	Sequence 44, Appl
27	48	29.6	15	1	US-10-495-664-1	Sequence 1, Appl
28	48	29.6	15	1	US-10-967-457-72	Sequence 72, Appl
29	48	29.6	15	1	US-10-839-799-111	Sequence 111, App
30	48	29.6	15	7	US-11-144-248-60	Sequence 60, Appl
31	48	29.6	20	7	US-11-065-943-48	Sequence 48, Appl
32	48	29.6	248	1	US-10-512-184-32	Sequence 32, Appl
33	48	29.6	251	1	US-10-512-184-30	Sequence 30, Appl
34	48	29.6	259	1	US-10-512-184-31	Sequence 31, Appl
35	48	29.6	259	1	US-10-512-184-33	Sequence 33, Appl
36	48	29.6	269	1	US-10-839-799-109	Sequence 109, App
37	48	29.6	313	1	US-10-512-184-72	Sequence 72, Appl
38	48	29.6	317	1	US-10-512-184-69	Sequence 69, Appl
39	48	29.6	320	1	US-10-512-184-67	Sequence 67, Appl
40	48	29.6	327	1	US-10-512-184-62	Sequence 62, Appl
41	48	29.6	328	1	US-10-512-184-63	Sequence 63, Appl
42	48	29.6	329	1	US-10-512-184-68	Sequence 68, Appl
43	48	29.6	329	1	US-10-512-184-70	Sequence 70, Appl
44	48	29.6	371	1	US-10-512-184-71	Sequence 71, Appl
45	48	29.6	465	1	US-10-967-648A-6	Sequence 6, Appl

## ALIGNMENTS

RESULT 1  
US-11-004-057-4  
; Sequence 4, Application US/11004057  
; Publication No. US20050244846A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Gary L.  
; TITLE OF INVENTION: MEK1 PROTEINS AND FRAGMENTS THEREOF FOR USE IN REGULATING  
; FILE REFERENCE: APOPTOSIS  
; FILE REFERENCE: CPI-042CPC  
; CURRENT APPLICATION NUMBER: US/11/004,057  
; CURRENT FILING DATE: 2004-12-02  
; PRIOR APPLICATION NUMBER: US/09/403,075  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 1493  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-004-057-4

Query Match 42.3%; Score 68.5; DB 7; Length 1493;  
Best Local Similarity 32.0%; Pred. No. 0.063;  
Matches 16; Conservative 4; Mismatches 11; Indels 19; Gaps 1;

Qy 1 AVSEIGGGGGGGGGLN-----SMERVEWLKKLQDV 31  
Db 20 ASPBAGGGGGGGGALQSGAPAGALLRPGSGRGRADRRRHVRKV 69

## RESULT 2

US-10-975-798-4  
; Sequence 4, Application US/10975798  
; Publication No. US20050250090A1  
; GENERAL INFORMATION:  
; APPLICANT: Edward Kaftan  
; APPLICANT: Adrienne Dubin  
; APPLICANT: Sandy Chaplan  
; TITLE OF INVENTION: ASSAY SYSTEMS AND METHODS FOR DETECTING MOLECULES THAT INTERACT  
; FILE REFERENCE: PRD2142  
; CURRENT APPLICATION NUMBER: US/10/975,798  
; CURRENT FILING DATE: 2004-10-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 579  
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-975-798-4
  Query Match      37.0%; Score 60; DB 1; Length 579;
  Best Local Similarity 46.2%; Pred. No. 0.27;
  Matches 12; Conservative 4; Mismatches 0; Gaps 0; Indels 10;
QY 6 GCGGGGGGGLNSMERVWLRKKLDV 31
Db 92 GCGGGGGGCHGSSGCTKSSKKKNQNI 117

RESULT 3
US-10-975-798-3
; Sequence 3, Application US/10975798
; Publication No. US20050250090A1
; GENERAL INFORMATION:
; APPLICANT: Edward Kaftan
; APPLICANT: Adrienne Dubin
; APPLICANT: Sandy Chaplan
; TITLE OF INVENTION: ASSAY SYSTEMS AND METHODS FOR DETECTING MOLECULES THAT INTERACT
; FILE REFERENCE: PRD2142
; CURRENT APPLICATION NUMBER: US/10/975,798
; PRIOR FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-798-3
  Query Match      37.0%; Score 60; DB 1; Length 580;
  Best Local Similarity 46.2%; Pred. No. 0.27;
  Matches 12; Conservative 4; Mismatches 0; Gaps 0; Indels 10;
QY 6 GCGGGGGGGLNSMERVWLRKKLDV 31
Db 93 GCGGGGGGCHGSSGCTKSSKKKNQNI 118

RESULT 4
US-11-004-057-21
; Sequence 21, Application US/11004057
; Publication No. US20050244846A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Gary L.
; TITLE OF INVENTION: APOPTOSIS
; FILE REFERENCE: CPT-042CPC
; CURRENT APPLICATION NUMBER: US/11/004,057
; CURRENT FILING DATE: 2004-12-02
; PRIOR FILING DATE: US/09/403,075
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 1493
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-004-057-21
  Query Match      34.9%; Score 56.5; DB 7; Length 1493;
  Best Local Similarity 34.8%; Pred. No. 1.8;
  Matches 16; Conservative 4; Mismatches 11; Indels 15; Gaps 2;
QY 1 AVSEITGGGG-----GGG-----GLNSMERVWLRKKLDV 31
Db 20 ASPEAGGGGGLQSGAPAGALLRRTSGRGRADRRRQLRKV 65

RESULT 5
US-10-957-569-64
; Sequence 64, Application US/10957569
; Publication No. US20050246785A1
; GENERAL INFORMATION:
; APPLICANT: COOK, Zhihong et al.
; TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
; FILE REFERENCE: 2750-1577EUS3
; CURRENT APPLICATION NUMBER: US/10/957,569
; CURRENT FILING DATE: 2004-09-30
; PRIOR FILING DATE: 2004-09-23
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-957-569-64
  Query Match      33.3%; Score 54; DB 1; Length 157;
  Best Local Similarity 42.9%; Pred. No. 0.39;
  Matches 12; Conservative 2; Mismatches 6; Indels 8; Gaps 1;
QY 6 GGGG-----GGGGGLNSMERVWLR 25
Db 76 GGGGARGGRSGRGGGGSSSRSDWKR 103

RESULT 6
US-10-841-129-7
; Sequence 7, Application US/10841129
; Publication No. US20050250113A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Ertenbach, Isolda
; APPLICANT: Hoon, Mark A.
; APPLICANT: Ryba, Nicholas J. P.
; APPLICANT: Zhang, Jifeng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: A Mammalian Magnesium/Manganese Sensing G Protein
; FILE REFERENCE: 02307E-145400US
; CURRENT APPLICATION NUMBER: US/10/841,129
; CURRENT FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:poly Gly
; OTHER INFORMATION: flexible linker
; NAME/KEY: MOD_RES
; LOCATION: (6)..(200)
; OTHER INFORMATION: Gly residues from position 6 to 200 may be present
; OTHER INFORMATION: or absent
US-10-841-129-7
  Query Match      33.3%; Score 54; DB 1; Length 200;
  Best Local Similarity 100.0%; Pred. No. 0.49;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GGGGGGGGG 14
Db 1 GGGGGGGGG 9
```

```

RESULT 7
US-11-060-659-32
; Sequence 32, Application US/11060659
; Publication No. US20050250163A1
; GENERAL INFORMATION:
; APPLICANT: Lorens, James
; APPLICANT: Holland, Sacha J.
; APPLICANT: Xu, Weiduan
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: Modulators of Angiogenesis and Tumorigenesis
; FILE REFERENCE: 021044-083310US
; CURRENT APPLICATION NUMBER: US/11/060,659
; CURRENT FILING DATE: 2005-02-16
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin ver. 2.1
; TITLE OF INVENTION: SH3 domain-binding protein 2
; TITLE OF INVENTION: (KIAA0660) CDNA
; TITLE OF INVENTION: SH3 domain-binding protein 2
; TITLE OF INVENTION: (KIAA0660) CDNA
; SEQ ID NO 32
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic poly
; OTHER INFORMATION: Gly flexible linker
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)..(200)
; OTHER INFORMATION: Gly residues from position 6 to 200 may be present
; OTHER INFORMATION: or absent
; US-11-060-659-32

```

```

Query Match 33.3%; Score 54; DB 7; Length 200;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 6 GGGGGGGGG 14
Db 1 GGGGGGGGG 9

```

```

RESULT 8
US-10-131-826A-532
; Sequence 532, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18

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; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 532
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-131-826A-532

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Query Match 33.3%; Score 54; DB 1; Length 269;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 6 GGGGGGGGG 14
Db 249 GGGGGGGGG 257

```

```

RESULT 9
US-11-065-943-20
; Sequence 20, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Thermus aquaticus
; US-11-065-943-20

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Query Match 33.3%; Score 54; DB 7; Length 562;
Best Local Similarity 50.0%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

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Qy 6 GGGGGGGGGLNSMERVEW 23
Db 5 GGGGGGGGSPKALBEAPW 22

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RESULT 10
US-11-065-943-22
; Sequence 22, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:

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; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426US0XCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; PRIOR FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Thermus aquaticus
; ORGANISM: Thermus aquaticus
US-11-065-943-22

Query Match      33.3%; Score 54; DB 7; Length 562;
Best Local Similarity 50.0%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 6 GGGGGGGGGLNSMERVEW 23
Db 5 GGGCGGGGSPKALEEAPW 22

RESULT 11
US-11-065-943-24
; Sequence 24, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426US0XCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; PRIOR FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Thermus aquaticus
; ORGANISM: Thermus aquaticus
US-11-065-943-24

Query Match      33.3%; Score 54; DB 7; Length 562;
Best Local Similarity 50.0%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 6 GGGGGGGGGLNSMERVEW 23
Db 5 GGGCGGGGSPKALEEAPW 22

RESULT 12
US-11-065-943-26
; Sequence 26, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426US0XCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; PRIOR FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Thermus aquaticus
; ORGANISM: Thermus aquaticus
US-11-065-943-30

Query Match      33.3%; Score 54; DB 7; Length 562;
Best Local Similarity 50.0%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 6 GGGGGGGGGLNSMERVEW 23
Db 5 GGGCGGGGSPKALEEAPW 22

RESULT 13
US-11-065-943-28
; Sequence 28, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426US0XCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; PRIOR FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Thermus aquaticus
; ORGANISM: Thermus aquaticus
US-11-065-943-28

Query Match      33.3%; Score 54; DB 7; Length 562;
Best Local Similarity 50.0%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 6 GGGGGGGGGLNSMERVEW 23
Db 5 GGGCGGGGSPKALEEAPW 22

RESULT 14
US-11-065-943-30
; Sequence 30, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426US0XCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; PRIOR FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30
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; LENGTH: 562
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-30

Query Match      33.3%; Score 54; DB 7; Length 562;
Best Local Similarity 50.0%; Pred. NO. 1.4;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 6 GGGGGGGGGLNSMERVIEW 23
    ||| ||| :|
Db 5 GGGCGGGGSPKALEAPW 22

RESULT 15
US-11-065-943-32
; Sequence 32, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USDXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-32

Query Match      33.3%; Score 54; DB 7; Length 562;
Best Local Similarity 50.0%; Pred. NO. 1.4;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 6 GGGGGGGGGLNSMERVIEW 23
    ||| ||| :|
Db 5 GGGCGGGGSPKALEAPW 22

Search completed: November 21, 2005, 16:34:56
Job time : 4.5 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:00:32 ; Search time 242.667 Seconds  
(without alignments)  
2554.189 Million cell updates/sec

Title: US-09-475-158A-14

Perfect score: 93

Sequence: 1 gcguuuccgaaucagcu.....guaaaaaacgagcagcuu 93

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq\_21.\*

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- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	100.0	93	3	AAA51729
2	83.4	89.7	93	3	AAA51730
3	73.8	79.4	93	3	AAA51731
4	71.2	76.6	152	2	AAT73910
5	69.6	74.8	102	12	ADG93179
6	69.6	74.8	102	12	ADJ65857
7	69.6	74.8	102	13	ADW14377
8	69.6	74.8	111	12	ADG93180
9	69.6	74.8	111	12	ADJ65858
10	69.6	74.8	111	13	ADW14375
11	69.6	74.8	117	12	ADG93260
12	69.6	74.8	168	2	AAT34865
13	69.6	74.8	252	12	ADG93181
14	69.6	74.8	252	12	ADJ65859
15	69.6	74.8	264	12	ADJ65913
16	69.6	74.8	276	12	ADJ65899
17	69.6	74.8	276	12	ADJ65899
18	69.6	74.8	276	12	ADJ87051
19	69.6	74.8	282	12	ADG93252

20	69.6	74.8	291	12	ADJ65901	ADJ65901 PTH DNA s
21	69.6	74.8	291	12	ADJ65900	ADJ65900 PTH DNA s
22	69.6	74.8	294	2	AAT34866	AAT34866 Plasmid p
23	69.6	74.8	321	12	ADJ65915	ADJ65915 Tandem po
24	69.6	74.8	420	12	ADJ65917	ADJ65917 Tandem po
25	69.6	74.8	426	12	ADJ65917	ADJ65917 Tandem po
26	69.6	74.8	528	6	AAS19702	AAS19702 Chimeric
27	68	73.1	108	13	ADV69494	ADV69494 Human par
28	68	73.1	114	13	ADV69502	ADV69502 Human par
29	68	73.1	489	12	ADG48030	ADG48030 Human PTH
30	68	73.1	489	12	ADG48059	ADG48059 Human PTH
31	68	73.1	489	12	ADG68786	ADG68786 Human mut
32	63.8	68.6	141	2	AAQ89920	AAQ89920 Recombina
33	63.8	68.6	141	2	AAQ89923	AAQ89923 rPTH codi
34	63.8	68.6	207	2	AAQ89923	AAQ89923 Expressio
35	62.2	66.9	145	13	ADW80822	ADW80822 DNA encod
36	60	64.5	405	3	AAA51452	AAA51452 PCpB-RVR-
37	60	64.5	408	3	AAA51455	AAA51455 PCpB-LVPR
38	60	64.5	408	3	AAA51454	AAA51454 PCpB-IEGR
39	60	64.5	411	3	AAA51453	AAA51453 PCpB-ALY-
40	60	64.5	414	3	AAA51456	AAA51456 PCpB-APR-
41	60	64.5	417	3	AAA51456	AAA51456 PCpB-VIPR
42	60	64.5	423	3	AAA51457	AAA51457 PCpB-DOVD
43	60	64.5	435	3	AAA51458	AAA51458 PCpB-DFIA
44	57.4	61.7	728	2	AAQ55301	AAQ55301 Truncated
45	57.4	61.7	945	2	AAQ55302	AAQ55302 gp55-Aen-

## ALIGNMENTS

RESULT 1	
AAA51729	
ID AAA51729 standard; RNA; 93 BP.	
XX	
AC AAA51729;	
DT 31-OCT-2000 (first entry)	
XX	
DE PTH functional domain conjugate peptide PCS coding sequence.	
XX	
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;	
KW resorption; remodeling; tether1; osteoporosis; ss.	
XX	
OS Homo sapiens.	
OS Synthetic.	
XX	
FH Key	Location/Qualifiers
FT CDS	1..93
FT	/*tag= a
FT	/product= "PCS"
XX	
PN WO200039278-A2.	
XX	
PD 06-JUL-2000.	
XX	
PF 30-DEC-1999; 99WO-US031108.	
XX	
PR 31-DEC-1998; 98US-0114577P.	
XX	
PA (GARD/) GARDELLA T J.	
PA (KRON/) KRONENBERG H M.	
PA (POTT/) POTTES J T.	
PA (JUEP/) JUEPPNER H.	
XX	
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;	
XX	
DR WPI; 2000-452384/39.	
DR P-PSDB; AAY96973.	
XX	
PT New compound comprising an amino terminal signaling functional domain	
PT linked to a carboxy-terminal binding portion of parathyroid hormone for	
PT treating mammalian conditions characterized by decreases in bone mass.	

PS  
XX  
Claim 14; Fig 1; 119pp; English.

Compounds of the structure or formula S-(L)<sub>n</sub>-B, R<sub>1</sub>-S-(L)<sub>n</sub>-R or S-(L)<sub>n</sub>-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R<sub>1</sub> is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing CAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHrp which avoids the need for regular injections to treat osteoporosis

[illegible]

RESULT 3  
AAA51731  
ID AAA51731 standard; RNA; 93 BP.  
XX  
XX  
AC AAA51731;  
AC  
XX  
DT 31-OCT-2000 (first entry)  
XX  
XX PTH functional domain conjugate peptide PG9 coding sequence.  
DE  
XX  
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;  
KW resorption; remodeling; tether1; osteoporosis; ss.  
KW

OS		Synthetic.	
XX	Key	Location/Qualifiers	
PH	CDS	1..93	
FT		/tag= a	
FT		/product= "PG9"	
XX	WO200039278-A2.		
PN			
XX	06-JUL-2000.		
PD			
XX			
PF	30-DEC-1999;	99WO-US031108.	
XX			
PR	31-DEC-1998;	98US-0114577P.	
XX	(GARD/) GARDELLA T J.		
PA	(KRON/) KRONENBERG H M.		
PA	(POTT/) POTTS J T.		
PA	(JUEP/) JUEPPNER H.		
XX			
PI	Gardella TJ, Kronenberg HM,	Potts JT, Jueppner H;	
XX			
WI	2000-452384/39.		
DR	P-PSDB; AAY96974.		
DR			

DR WFI; 2000-452384/39.  
DR P-PSDB; AAY96974.





DR P-PSDB; ADG93159.

XX New expression cassette comprising an operably linked nucleic acid

PT sequence, useful for producing a tandem polypeptide that forms an

PT inclusion body when expressed in a cell.

XX

PS Disclosure; SEQ ID NO 60; 157pp; English.

XX

CC This invention relates to a novel expression cassette and methods for

CC high yield production of polypeptides. The cassette comprises an operably

CC linked nucleic acid sequence, where the expression of the cassette

CC produces a tandem polypeptide that forms an inclusion body when expressed

CC in a cell. The expression cassette is useful for producing peptide and

CC polypeptide in a cell, preferably a tandem polypeptide that forms an

CC inclusion body when expressed in a cell. The present sequence is that of

CC a DNA sequence which encodes a polypeptide which may be produced using

CC the expression cassette of the invention.

XX

XX Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;

SEQ

Query Match 74.8%; Score 69.6; DB 12; Length 102;

Best Local Similarity 63.0%; Pred. No. 1.9e-14;

Matches 58; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

Oy 2 CUGUUUCGAAAUCCAGCUGAUGCAGCGUGUGUGUGUGUGAUCUCCAUUGGAACGUG 61

Db 2 CTGTTTCTGAAATCCAGCTGATGCACAACTGGTGAACACCTCTATGGAACGTT 61

Oy 62 UUGAAUGCGUGCGUAAAAAACCUGCAGGACGUU 93

Db 62 TTGAATGGCTGCGTAAATAAACTGCAGGACGTT 93

RESULT 6

ADJ65857

ID ADJ65857 standard; DNA; 102 BP.

AC ADJ65857;

XX

DT 06-MAY-2004 (first entry)

XX

DE PTH peptide coding sequence #1.

XX

XX expression cassette; tandem polypeptide; inclusion body;

KW inclusion body fusion partner; PTH; gene; ds.

XX

OS Unidentified.

XX

PN WO200310022-A2.

XX

PD 04-DEC-2003.

XX

XX 23-MAY-2003; 2003WO-US016645.

XX

PR 24-MAY-2002; 2002US-0383212P.

XX

PA (REST-) RESTORAGEN INC.

XX

PI Xia Y, Peng L;

XX

DR WPI; 2004-035129/03.

DR P-PSDB; ADJ65837.

XX

XX New expression cassette comprising an operably linked nucleic acid

PT sequence, useful for producing a tandem polypeptide that forms an

PT inclusion body when expressed in a cell.

XX

PS Disclosure; SEQ ID NO 33; 132pp; English.

XX

CC The invention comprises an expression cassette which produces a tandem

CC polypeptide that form an inclusion body when expressed in a cell. The

CC expression cassette of the invention is useful for producing a peptide or

CC polypeptide in a cell, preferably a tandem polypeptide that forms an

CC

CC inclusion body when expressed in a cell. The present DNA sequence encodes

CC a peptide which may be used in the construction of a tandem polypeptide

CC of the invention.

XX

XX Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;

SEQ

Query Match 74.8%; Score 69.6; DB 12; Length 102;

Best Local Similarity 63.0%; Pred. No. 1.9e-14;

Matches 58; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

Oy 2 CUGUUUCGAAAUCCAGCUGAUGCAGCGUGUGUGUGUGAUCUCCAUUGGAACGUG 61

Db 2 CTGTTTCTGAAATCCAGCTGATGCACAACTGGTGAACACCTCTATGGAACGTT 61

Oy 62 UUGAAUGCGUGCGUAAAAAACCUGCAGGACGUU 93

Db 62 TTGAATGGCTGCGTAAATAAACTGCAGGACGTT 93

RESULT 7

ADJ14377

ID ADJ14377 standard; DNA; 102 BP.

AC ADJ14377;

XX

XX 10-MAR-2005 (first entry)

XX

DE Human parathyroxin PTH 1-34 peptide encoding DNA SEQ ID NO:3.

XX

XX ds; parathyroxin; recombinant protein; protein engineering.

KW

XX Homo sapiens.

OS

XX CN1424325-A.

PN

PD 18-JUN-2003.

XX

XX 12-DEC-2001; 2001CN-00142627.

PF

XX 12-DEC-2001; 2001CN-00142627.

PR

XX (SHAN-) SHANGHAI BIOLOGICAL ENG RES CENT ACAD S.

PA

PI Chen C, Xiu C, Li M;

XX

XX WPI; 2004-099606/11.

DR P-PSDB; ADJ14378.

XX

XX Production of reorganized human parathyroid hormone 1-34 peptide.

PT

XX Disclosure; SEQ ID NO 3; 25pp; Chinese.

PS

XX

XX The invention relates to a novel process for preparing recombinant human

CC parathyroxin 1-34 peptide, including such steps as culturing a host cell

CC in proper conditions, separating Gly-Ser-Pro-PTH 1-34 peptide (ADJ14376),

CC severing by pro endopeptidase to form PTH 1-34 peptide (ADJ14378) and

CC separating and purifying PTH 1-34 peptide. The present sequence encodes

CC the PTH 1-34 peptide.

XX

XX Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;

SEQ

Query Match 74.8%; Score 69.6; DB 13; Length 102;

Best Local Similarity 63.0%; Pred. No. 1.9e-14;

Matches 58; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

Oy 2 CUGUUUCGAAAUCCAGCUGAUGCAGCGUGUGUGUGUGAUCUCCAUUGGAACGUG 61

Db 2 CTGTTTCTGAAATCCAGCTGATGCACAACTGGTGAACACCTCTATGGAACGTT 61

Oy 62 UUGAAUGCGUGCGUAAAAAACCUGCAGGACGUU 93

Db 62 TTGAATGGCTGCGTAAATAAACTGCAGGACGTT 93

[illegible]







GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:35:17 ; Search time 1177.67 Seconds  
(without alignments)  
4488.911 Million cell updates/sec

Title: US-09-475-158A-14  
Perfect score: 93  
Sequence: 1 gcguuuuccgaaauccagcu.....guaaaaaacugcaggagcuu 93

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: gb\_in.\*
- 3: gb\_env.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pr.\*
- 9: gb\_ro.\*
- 10: gb\_ats.\*
- 11: gb\_sy.\*
- 12: gb\_un.\*
- 13: gb\_vi.\*
- 14: gb\_htg.\*
- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	93	100.0	93	6	BD266832 PTH funct
2	83.4	89.7	93	6	BD266833 PTH funct
3	73.8	79.4	93	6	BD266834 PTH funct
4	66.4	71.4	258	6	AR269042 Sequence
5	63.8	68.6	141	6	AR005132 Sequence
6	63.8	68.6	141	6	AR005133 Sequence
7	63.8	68.6	141	6	AR177779 Sequence
8	63.8	68.6	141	6	AR177780 Sequence
9	63.8	68.6	141	6	AR043797 Sequence
10	60	64.5	405	6	BD234383 Recombina
11	60	64.5	408	6	BD234385 Recombina
12	60	64.5	408	6	BD234386 Recombina
13	60	64.5	411	6	BD234384 Recombina
14	60	64.5	414	6	BD234390 Recombina
15	60	64.5	417	6	BD234387 Recombina
16	60	64.5	423	6	BD234388 Recombina
17	60	64.5	435	6	BD234389 Recombina
18	57.4	61.7	717	6	A36847 Sequence 1

19	57.4	61.7	945	6	A36849	A36849 Sequence 3
20	54.2	58.3	252	6	AR027046	AR027046 Sequence
21	54.2	58.3	252	6	E05675	E05675 DNA encodin
22	52.6	56.6	252	6	AR027011	AR027011 Sequence
23	52.6	56.6	252	6	AR027044	AR027044 Sequence
24	52.6	56.6	252	6	AR030635	AR030635 Sequence
25	52.6	56.6	252	6	AR168173	AR168173 Sequence
26	52.6	56.6	252	6	E05658	E05658 DNA encodin
27	52.6	56.6	252	6	E05673	E05673 DNA encodin
28	52.6	56.6	252	6	I83594	I83594 Sequence 1
29	52.6	56.6	263	6	AR027020	AR027020 Sequence
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31	52.6	56.6	263	6	E05671	E05671 DNA encodin
32	52.6	56.6	263	6	I83595	I83595 Sequence 3
33	52.6	56.6	263	11	S71759	S71759 human parat
34	52.6	56.6	265	6	AR027021	AR027021 Sequence
35	52.6	56.6	265	6	E05672	E05672 DNA encodin
36	52.6	56.6	265	6	I83596	I83596 Sequence 4
37	51	54.8	102	6	BD170195	BD170195 Process f
38	51	54.8	186	6	BD170222	BD170222 Process f
39	51	54.8	201	6	BD170213	BD170213 Process f
40	51	54.8	225	6	BD170211	BD170211 Process f
41	51	54.8	240	6	BD170198	BD170198 Process f
42	51	54.8	252	6	AR027050	AR027050 Sequence
43	51	54.8	252	6	BD170196	BD170196 Process f
44	51	54.8	252	6	E05677	E05677 DNA encodin
45	51	54.8	258	6	BD140917	BD140917 Process f

## ALIGNMENTS

RESULT 1	BD266832	93 bp	RNA	linear	PAT 17-JUL-2003
LOCUS	PTH functional domain conjugate peptides, novel tethered ligand-receptor molecules.				
DEFINITION	BD266832				
ACCESSION	BD266832.1	GI:33076600			
VERSION	JP 2002533115-A/1.				
KEYWORDS	synthetic construct				
SOURCE	other sequences; artificial sequences.				
ORGANISM	1 (bases 1 to 93)				
REFERENCE	Gardella, T.J., Kronenberg, H.M., Potts, J.T. and Jueppner, H.				
AUTHORS	PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules				
TITLE	Patent: JP 2002533115-A 1 08-OCT-2002;				
JOURNAL	THE GENERAL HOSPITAL CORP				
COMMENT	OS Artificial Sequence				
	PN JP 2002533115-A/1				
	PD 08-OCT-2002				
	PF 30-DEC-1999 JP 2000591171				
	PR 31-DEC-1998 US 60/114577				
	PI THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD PI JUEPPNER				
	PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P5/18, A61P19/08, PC A61P19/10,				
	PC A61P43/00, C07K14/635, C07K14/72, C07K19/00, C12N1/15, C12N1/19, PC C12N1/21,				
	PC C12N5/10, G01N33/15, G01N33/50, C12N15/00, C12N5/00, A61K37/02 CC Description of Artificial Sequence: modified PTH sequence PTH Key				
	FT source 1..93				
	FT Location/Qualifiers				
	Location/Qualifiers				
	1..93				
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	/mol_type="genomic RNA"				
	/db_xref="taxon:32630"				
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 93;	DB 6;	Length 93;	





RESULT 6			
AR005133/c			
LOCUS	AR005133	141 bp	DNA
DEFINITION	Sequence 5 from patent US 5747453.		linear
ACCESSION	AR005133		
VERSION	AR005133.1	GI:3966012	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 141)		
TITLE	Holladay, L.A. and Oidenburg, K.R.		
JOURNAL	Method for increasing the electrotransport flux of polypeptides		
FEATURES	Patent: US 5747453-A 5 05-MAY-1996;		
source	LOCUS/Qualifiers		
	1..141		

[illegible]

RESULT 7	AR177779	141 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	AR177779				
DEFINITION	Sequence 3 from patent US 6313092.				
ACCESSION	AR177779				
VERSION	AR177779.1	GI:17920134			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 141)				
TITLE	Holladay,L.A. and Oldenburg,K.R.				
JOURNAL	Method for increasing the electrotransport flux of polypeptides				
FEATURES	Patent: US 6313092-A3 06-NOV-2001;				
	location/Qualifiers				
	1..141				
source	/organism="unknown" /mol_type="unassigned DNA"				

[illegible]

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SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 141)
AUTHORS     Holladay,L.A. and Oldenburg,X.R.
TITLE       Method for increasing the electrotransport flux of polypeptides
JOURNAL     Patent: US 6313092-A 5 06-NOV-2001;
FEATURES
            Location/Qualifiers
                1..141
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Source	Unknown
ORGANISM	Unknown
REFERENCE	Unclassified
AUTHORS	1 (bases 1 to 207)
TITLE	Oldenburg, K.R. and Selick, H.E.
JOURNAL	Compounds with FTH activity
FEATURES	Patent: US 5814603-A 8, 29-SEP-1998;
Source	Location/Qualifiers
	1..207
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	/mol_type="unassigned DNA"
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Best Local Similarity	61.5%; Pred. No. 1.2e-10;
Matches	56; Conservative 18; Mismatches 17; Indels 0; Gaps 0;
Oy	2 CUGUUGCCGAUAUCCAGCUGAUGCAGCGUGUGUGUGUGUGUGAUCUCCAUAGAAGCG 61
Db	71 CCGTTCCGAATCCAGCGCTGCGACCAACCTGGGTAAACCTGAACCTCCCTGAGCG 130
Oy	62 UUGAUGGCGUGGUAUAAACUGCGAGCGU 92
Db	131 TTGAATGCTGCTGCTAAGAAACGCGAGCGAT 161
RESULT 10	
LOCUS	BD234383 405 bp DNA linear PAT 17-JUL-2003
DEFINITION	Recombinant synthesis of beta-1ipotropan and other peptides.
ACCESSION	BD234383
VERSION	BD234383.1 GI:33044153
KEYWORDS	JP 2002533072-A/4.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	Other sequences; artificial sequences.
AUTHORS	1 (bases 1 to 405)
TITLE	Hale, J.E., Hersheberger, C.T., Larson, J.L. and Menke, M.A.
JOURNAL	Recombinant synthesis of beta-1ipotropan and other peptides
COMMENT	Patent: JP 2002533072-A 4 08-OCT-2002;
	ELI LILLY AND CO
OS	Artificial Sequence
PN	JP 2002533072-A/4
PD	08-OCT-2002
PF	15-DEC-1999 JP 2000589671
PR	21-DEC-1998 US 60/113058
PI	JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON,
	MICHAEL ANDREW MENKE
PC	C12N15/09, C07K14/67, C07K19/00, C12N1/15, C12N1/19, C12N1/21 PC
	C12N5/10 C12N9/50
CC	C12P21/02, C12N15/00, C12N5/00
Key	Description of Artificial Sequence: PCpB-RVR-hPTH fusion FH
FT	Location/Qualifiers
	(4)..(393).
FEATURES	
Source	Location/Qualifiers
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Best Local Similarity	57.6%; Pred. No. 2.5e-09;
Matches	53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
Oy	2 CUGUUGCCGAUAUCCAGCUGAUGCAGCGUGUGUGUGUGUGAUCUCCAUAGAAGCG 61
Db	293 CCGTTCCGAATCCAGCGCTGCGACCAACCTGGGTAAACCTGAACCTCCCTGAGCG 352
Oy	62 UUGAUGGCGUGGUAUAAACUGCGAGCGU 93
Db	353 TTGAATGCTGCTGCTAAGAAACGCGAGCGAT 384

RESULT 11	BD234385	408 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD234385				
DEFINITION	Recombinant synthesis of beta-lipotropin and other peptides.				
ACCESSION	BD234385.1	GI:33044155			
VERSION	JP 2002533072-A/6.				
KEYWORDS	JP 2002533072-A/6.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	other sequences; artificial sequences.				
AUTHORS	1 (bases 1 to 408)				
TITLE	Hale,J.E., Hershsberger,C.L., Larson,J.L. and Menke,M.A.				
JOURNAL	Recombinant synthesis of beta-lipotropin and other peptides				
COMMENT	Patent: JP 2002533072-A 6 08-OCT-2002;				
	ELI LILLY AND CO				
	OS Artificial Sequence				
	PN JP 2002533072-A/6				
	PD 08-OCT-2002				
	PF 15-DEC-1999 JP 2000589671				
	PR 21-DEC-1998 US 60/113058				
	P1 JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,				
	P1 MICHAEL ANDREW MENKE				
	PC C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC				
	PC C12M5/10,C12M9/50				
	CC C12P21/02,C12N15/00,C12M5/00				
	CC Description of Artificial Sequence: PCPB-1EGR-hPTH fusion FH				
	Key Location/Qualifiers				
	FT CDS	Location/Qualifiers			
		(4)..(396).			
FEATURES	Location/Qualifiers				
source	1..408				
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	/mol_type="genomic DNA"				
	/db_xref="taxon:32630"				
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Query Match	64.5%; Score 60; DB 6; Length 408;				
Best Local Similarity	57.6%; Pred. No. 2.5e-09;				
Matches	53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;				
Oy	2 CUGUUCGCCAAUCCAGCUGACGAGUGAGUGUGUCUGACUCCAGCAACUGAACGUG 61				
Db	296 CUGTTTCGAAATCCAGCTGATGATACCGGGGCAAACTGACCTATGAGCGCG 355				
Oy	62 UUGAUGGCGGUAUAAACUGACGACGACU 93				
Db	356 TAGAATGGCTGCTGTAAGAACTGACGATGTT 387				
RESULT 12					
BD234386					
LOCUS	BD234386	408 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Recombinant synthesis of beta-lipotropin and other peptides.				
ACCESSION	BD234386				
VERSION	BD234386.1	GI:33044156			
KEYWORDS	JP 2002533072-A/7.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	other sequences; artificial sequences.				
AUTHORS	1 (bases 1 to 408)				
TITLE	Hale,J.E., Hershsberger,C.L., Larson,J.L. and Menke,M.A.				
JOURNAL	Recombinant synthesis of beta-lipotropin and other peptides				
COMMENT	Patent: JP 2002533072-A 7 08-OCT-2002;				
	ELI LILLY AND CO				
	OS Artificial Sequence				
	PN JP 2002533072-A/7				
	PD 08-OCT-2002				
	PF 15-DEC-1999 JP 2000589671				
	PR 21-DEC-1998 US 60/113058				
	P1 JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,				
	P1 MICHAEL ANDREW MENKE				
	PC C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC				
	PC C12M5/10,C12M9/50,				

PC C12P21/02.C12N15/00.C12N5/00  
CC Description of Artificial Sequence: PCPB-LVPR-hPTH fusion FH  
KEY Location/Qualifiers  
FT CDS (4)..(396).

FEATURES  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

## ORIGIN

Query Match 64.5%; Score 60; DB 6; Length 408;  
Best Local Similarity 57.6%; Pred. No. 2.5e-09;  
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY 2 CUGUUCGGAUUCAGCUGAUGCAGUGUGUGUGUCUGAUCUCCAGGAACGUG 61  
DB 296 CTGTTTCTGAAATCCAGCTGATGCACTAACCTGGCAACATCTGAACCTATGAGGCGTG 355

QY 62 UUGAUGGCGUGGUAUAAACUGCAGGACGU 93  
DB 356 TAGAATGCGTGGTAAGAGCTGCAGAGATT 387

RESULT 13  
BD234384 411 bp DNA linear PAT 17-JUL-2003  
LOCUS  
DEFINITION Recombinant synthesis of beta-lipotropin and other peptides.  
ACCESSION BD234384.1 GI:33044154  
VERSION JP 2002533072-A/5.  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences: artificial sequences.

REFERENCE  
AUTHORS Hale,J.E., Hersberger,C.L., Larson,J.L. and Menke,M.A.  
TITLE Recombinant synthesis of beta-lipotropin and other peptides  
JOURNAL Patent: JP 2002533072-A 5 08-OCT-2002;  
ELI LILLY AND CO  
OS Artificial Sequence  
PN JP 2002533072-A/5  
PD 08-OCT-2002  
PF 15-DEC-1999 JP 2000589671  
PR 21-DEC-1998 US 60/113058  
PI JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,  
PI MICHAEL ANDREW MENKE  
PC C12N15/09.C07K14/67.C07K19/00.C12N1/15.C12N1/19.C12N1/21 PC  
,C12N5/10.C12N9/50,  
PC C12P21/02.C12N15/00.C12N5/00  
CC Description of Artificial Sequence: PCPB-ALV-hPTH fusion FH  
KEY Location/Qualifiers  
FT CDS (4)..(399).

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/db\_xref="taxon:32630"

## ORIGIN

Query Match 64.5%; Score 60; DB 6; Length 411;  
Best Local Similarity 57.6%; Pred. No. 2.5e-09;  
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY 2 CUGUUCGGAUUCAGCUGAUGCAGUGUGUGUGUCUGAUCUCCAGGAACGUG 61  
DB 299 CTGTTTCTGAAATCCAGCTGATGCACTAACCTGGCAACATCTGAACCTATGAGGCGTG 358

QY 62 UUGAUGGCGUGGUAUAAACUGCAGGACGU 93  
DB 359 TAGAATGCGTGGTAAGAGCTGCAGAGATT 390

RESULT 14

BD234390 414 bp DNA linear PAT 17-JUL-2003  
LOCUS  
DEFINITION Recombinant synthesis of beta-lipotropin and other peptides.  
ACCESSION BD234390  
VERSION BD234390.1 GI:33044160  
KEYWORDS JP 2002533072-A/11.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences: artificial sequences.

REFERENCE  
AUTHORS Hale,J.E., Hersberger,C.L., Larson,J.L. and Menke,M.A.  
TITLE Recombinant synthesis of beta-lipotropin and other peptides  
JOURNAL Patent: JP 2002533072-A 11 08-OCT-2002;  
ELI LILLY AND CO  
OS Artificial Sequence  
PN JP 2002533072-A/11  
PD 08-OCT-2002  
PF 15-DEC-1999 JP 2000589671  
PR 21-DEC-1998 US 60/113058  
PI JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,  
PI MICHAEL ANDREW MENKE  
PC C12N15/09.C07K14/67.C07K19/00.C12N1/15.C12N1/19.C12N1/21 PC  
,C12N5/10.C12N9/50,  
PC C12P21/02.C12N15/00.C12N5/00  
CC Description of Artificial Sequence: PCPB-APR-hPTH fusion FH  
KEY Location/Qualifiers  
FT CDS (4)..(402).

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/db\_xref="taxon:32630"

## ORIGIN

Query Match 64.5%; Score 60; DB 6; Length 414;  
Best Local Similarity 57.6%; Pred. No. 2.5e-09;  
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY 2 CUGUUCGGAUUCAGCUGAUGCAGUGUGUGUGUCUGAUCUCCAGGAACGUG 61  
DB 302 CTGTTTCTGAAATCCAGCTGATGCACTAACCTGGCAACATCTGAACCTATGAGGCGTG 361

QY 62 UUGAUGGCGUGGUAUAAACUGCAGGACGU 93  
DB 362 TAGAATGCGTGGTAAGAGCTGCAGAGATT 393

RESULT 15

BD234387 417 bp DNA linear PAT 17-JUL-2003  
LOCUS  
DEFINITION Recombinant synthesis of beta-lipotropin and other peptides.  
ACCESSION BD234387  
VERSION BD234387.1 GI:33044157  
KEYWORDS JP 2002533072-A/8.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences: artificial sequences.

REFERENCE  
AUTHORS Hale,J.E., Hersberger,C.L., Larson,J.L. and Menke,M.A.  
TITLE Recombinant synthesis of beta-lipotropin and other peptides  
JOURNAL Patent: JP 2002533072-A 8 08-OCT-2002;  
ELI LILLY AND CO  
OS Artificial Sequence  
PN JP 2002533072-A/8  
PD 08-OCT-2002  
PF 15-DEC-1999 JP 2000589671  
PR 21-DEC-1998 US 60/113058  
PI JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,  
PI MICHAEL ANDREW MENKE  
PC C12N15/09.C07K14/67.C07K19/00.C12N1/15.C12N1/19.C12N1/21 PC  
,C12N5/10.C12N9/50,  
PC C12P21/02.C12N15/00.C12N5/00  
CC Description of Artificial Sequence: PCPB-VIPR-hPTH fusion FH

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Key          Location/Qualifiers
FEATURES     FT      CDS           (4)..(405).
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ORIGIN

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Query Match      64.5%; Score 60; DB 6; Length 417;
Best Local Similarity 57.6%; Pred. No. 2.5e-09;
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

OY      2  CUGUUCCGAUUCACUCUGAUGCAGGUGUGUGUGUCUGAACUCCAUAGGAGUG 61
         ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      305 CTGTTCTGAATCGAGTGTGATGCAATAACCTGGGCMAACATCTGAACTTATGAGCGTG 364

OY      62  UUGAUGGUCUGCGUAAAAACUCAGCAGACGU 93
         :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      365 TAGAATGGCTGCTAAGAAAGCTGACGAGATGTT 396

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Search completed: November 23, 2005, 23:59:13  
 Job time : 1179.67 secs



Site 2: Eco RI; 1st strand cDNA was primed with a Not I -  
 oligo(dT) primer  
 15'-TGTACCAATCTGAAGTGGAGCGCGCCGACCAATTTTTTTTTTTTTTTT  
 TTTT-3', double-stranded cDNA was size selected, ligated  
 to Eco RI adapters (Pharmacia), digested with Not I and  
 cloned into the Not I and Eco RI sites of a modified pT73  
 vector (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid  
 adenomas was kindly provided by Dr. Stephen Marx, National  
 Institute of Diabetes and Digestive and Kidney Diseases,  
 NIH."

## ORIGIN

Query Match 52.0%; Score 48.4; DB 8; Length 324;  
 Best Local Similarity 53.8%; Pred. No. 2.9e-05;  
 Matches 49; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

OY 2 CUGUUCGGAUCCAGCUGAUGCAGGUGUGUGUGUGUUAUCCUAGAGCG 61  
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 Db 60 CTGTAGTGAATACAGCTTATGATCACTTGAGAAAACATCTGAATCGATGAGAG 119  
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 OY 62 UUGAAUGGCGUGUAAAAAACUGCAGAGCGU 92  
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 Db 120 TAGAATGGCTGCTGTAAGAACTGCAGATGT 150

RESULT 2 352 bp mRNA linear EST 15-MAY-1996  
 W39062 zB34c06.r1 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone  
 LOCUS IMAGE:305482 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR  
 DEFINITION (HUMAN); mRNA sequence.

ACCESSION W39062.1 GI:1320771  
 VERSION EST  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo

REFERENCE 1 (bases 1 to 352)  
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
 Trevaaskis,E., Waterston,R., Williamson,A., Woldmann,F. and  
 Wilson,R.

TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu

This clone is available royalty-free through LIND; contact the  
 IMAGE Consortium (info@image.lind.gov) for further information.  
 Seg primer: mob.REGA+ET  
 High quality sequence stop: 286.  
 Location/Qualifiers

## FEATURES

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 /dev\_stage="adult"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_id="Soares\_parathyroid\_tumor\_NBHPA"  
 /note="Organ: parathyroid gland; Vector: pT73D  
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 Site\_2: Eco RI; 1st strand cDNA was primed with a Not I -

## ORIGIN

Query Match 51.4%; Score 47.8; DB 8; Length 352;  
 Best Local Similarity 53.8%; Pred. No. 4.7e-05;  
 Matches 49; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

OY 2 CUGUUCGGAUCCAGCUGAUGCAGGUGUGUGUGUGUUAUCCUAGAGCG 61  
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 OY 62 UUGAAUGGCGUGUAAAAAACUGCAGAGCGU 92  
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 245 TAGAATGGCTGCTGTAAGAACTGCAGATGT 275

RESULT 3 376 bp mRNA linear EST 15-MAY-1996  
 W38966 zB28b12.r1 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone  
 LOCUS IMAGE:304895 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR  
 DEFINITION (HUMAN); mRNA sequence.

ACCESSION W38966.1 GI:1320674  
 VERSION EST  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo

REFERENCE 1 (bases 1 to 376)  
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
 Trevaaskis,E., Waterston,R., Williamson,A., Woldmann,F. and  
 Wilson,R.

TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu

This clone is available royalty-free through LIND; contact the  
 IMAGE Consortium (info@image.lind.gov) for further information.  
 Seg primer: mob.REGA+ET  
 Location/Qualifiers

## FEATURES

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 /mol\_type="mRNA"  
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 /dev\_stage="adult"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_id="Soares\_parathyroid\_tumor\_NBHPA"  
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 Site\_2: Eco RI; 1st strand cDNA was primed with a Not I -  
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 15'-TGTACCAATCTGAAGTGGAGCGCGCCGACCAATTTTTTTTTTTTTTTT



oligo(4T) primer  
[5'-TCCTACCAATCCAAAGTGAGAGCGGCCACCACAATTGTTTTTTTTTTTTTTT  
TTTT-3'], double-stranded cDNA was size selected, ligated to  
Eco RI adapters (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of a modified pTV73  
vector (Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fátima Bonaldo. RNA from sporadic parathyroid  
adenomas was kindly provided by Dr. Stephen Marx, National  
Institute of Diabetes and Digestive and Kidney Diseases,  
NIH."

## ORIGIN

Query Match 51.4%; Score 47.8; DB 8; Length 434;  
 Best Local Similarity 53.8%; Pred. No. 4.8e-05;  
 Matches 49; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

[illegible]

RESULT 7  
W56235

LOCUS	450 bp	mRNA	linear	EST 10-OCT-1996
DEFINITION	W56235			
DESCRIPTION	zgc1e11.r1 Soares parathyroid tumor NbhPA Homo sapiens cDNA clone			
FEATURES	IMAGE:321068.5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN) ;, mRNA sequence.			

KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE  
1 (bases 1 to 450)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Hominidae, Homo.

TITLE	JOURNAL	COMMENT
The WashU-Merck EST Project	Unpublished (1995)	Contact: Wilson RK

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewartson.wustl.edu  
This clone is available royalty-free through LML : com  
IMAGE Consortium (info@image.llnl.gov) for further info  
Insert length: 865  
Seq Error: 0.00  
Seq primer: mbd.REG+57.  
Location/Qualifiers  
1..450

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/mol_type="mRNA"
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/db_xref="Ensembl:ENST00000265286"
/clone_id="Soares.parathyroid.tumor.NbHPa"
/name="Organ. parathyroid gland; Vector: pTR73D
(pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(27) primer

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ORIGIN

Query Match	51.4%	Score 47.8;	DB 8;	Length 496;
Best Local Similarity	53.8%	Pred. No. 5e-05;		
Matches	49;	Conservative	15;	Mismatches 27;
				Indels 0;
				Gaps 0.

15'-TGGTACCAATCTAAGTCGAGCGCCGACCAATTCTTTTCTTTTTTT  
TTT-3'), double-stranded cDNA was size selected, ligated  
to Eco RI adapters (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of a modified p73m3  
vector (Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fátima Bonalolo. RNA from sporadic parathyroid  
adenomas was kindly provided by Dr. Stephan Marx, National  
Institute of Diabetes and Digestive and Kidney Diseases,  
NIH."

[illegible]

RESULT 10	LOCUS	DEFINITION
W19765	536 bp	linear EST 03-MAY-1996
W19765		2b39c403.r1 Soares parathyroid tumor NblpA Homo sapiens cDNA clone
		(IMAGE:305996.5) similar to gb:v00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.

ORIGIN

Query Match	51.4%	Score 47.8;	DB 8;	length 536;
Best Local Similarity	53.8%;	Pred. No. 5e-05;		
Matches	49;	Conservative	15;	Mismatches 27;
			Indels	0;
			Gaps	0;

PT773-3.) double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT731 vector (Pharmacia). Library was through one round of normalization to a cot = 5. Library constructed by Bento Soares and M. Patricia Bernaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH.<sup>11</sup>

[illegible]

RESULT 11	W56120	LOCUS	DEFINITION
576 bp	W56120	576 bp	576 bp
linear	z56106.x1	linear	linear
EST 11-OCT-1996	Soares parathyroid tumor NHPPA Homo sapiens cDNA clone	EST 11-OCT-1996	EST 11-OCT-1996
	IMAGE:336383.5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.		



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Page 8

Db		112 CTGTGAGTGAATAACAGCTTTATGCATTAACCTTGCGAAAACACTTGAACTCGATGGAGAAG 171
Qy	62 UUGAAGUCUCCGUAAAAAACUCGACGACU 92	
	:    ::   ::   ::   ::   ::   :	
Db	172 TAGAATGCTCCTCGTAAGACCTCGACGAGAT 202	

RESULT 14	LOCUS	DEFINITION
AI051997/c	AI051997	741 bp -mRNA linear, EST 10-JUL-1998 cy229c05.x1 Soares parathyroid tumor NBIPA Homo sapiens cDNA clone IMAGE:1667240.3, similar to gb:V00537 PARATHYROID HORMONE PRECURSOR (HUMAN) ;, mRNA sequence.

ACCESSION	AI051997	
VERSION	AI051997.1	GI:3307988
KEYWORDS	EST.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

REFERENCE	1 (bases 1 to 741)
AUTHORS	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: CGabbs-r@mail.nih.gov  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: [www.bio.lnlnl.gov/bbrp/image/image.html](http://www.bio.lnlnl.gov/bbrp/image/image.html)  
Seq primer: -40m13 fwd. EP from Amersham  
High quality sequence stop: 444.

FEATURES	Location/Qualifiers
source	1. .741

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/clone="IMAGE:1667240"
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/lab_host="DH10B (ampicillin resistant)"
/clone_1ib="Soares parathyroid tumor NBHPA"
/note="Organ: Parathyroid Gland; Vector: pT73D
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
o1gg(dT) primer
15'-GTTACCAATCGACAGCGGCGGCGACCAATTTTTTTTTTTTTTTTTT-3'
TTTTT-3'], double-stranded cDNA was site selected, ligated
to Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT73
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Palma Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

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## ORIGIN

	Query Match	51.4%	Score 47.8	DB 1	Length 741;
	Best Local Similarity	53.8%	Pred. No. 5	3e-05;	
	Matches	49,	Conservative	15,	Mismatches 27; Indels 0; Gaps 0;
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Dd	618	CCTGTACTAAATTAACGCTTAGCTTAAACCGGGAAAACTCTGAATCTGAATCGAGAG	559		
QY	62	TUAGAACGUCGCUAAAAAACGACGACGCU	92		

Db	558	TAGAAATGCGTGGCTGACAGAGCTG	528
RESULT 15			
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LOCUS			EST 06-FEB-2003
DEFINITION			
	EX106223	Scarsa_parethyroid_tumor NBH9A Homo sapiens	cDNA clone
	IMAGE324728	IMAGE:321911, mRNA sequence.	

ACCESSION	EX106232
VERSION	GI:27846872
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 757)	Eberl, L., Heil, O., Hennig, S., Neubert, P., Patsch, E., Peters, M., Raderhof, U., Schneider, D., and Korn, B.	Human Unigeneset - RZPp3	Unpublished (2003)	Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD: IMAGP98BJ24728.  
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No. 972)  
<http://www.rzpd.de/ClonedCards/cgi-bin/showlib.pl/cgi/response?libNo=972> Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heidenbergstr. 6 D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
[www.rzpd.de](http://www.rzpd.de)  
This clone is available royalty-free from RZPD.  
Contact RZPD ([clone@rzpd.de](mailto:clone@rzpd.de)) for further information. Seq primer:  
M13r. Primer sequence: TTTCACACAGGAGACGCTGTGAC.

FEATURES	Location/Qualifiers
source	1. .757

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/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_id="Soares parathyroid tumor NbHPa"
/note="Organ: parathyroid gland; Vector: pT73D
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo (dT) primer
15'-GTATACCAATCATGAATGTGGAGCGGCGGACACCAATTTTTTTTTTTTTTTT
TTTT-3', double-stranded cDNA was size selected, ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT733
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

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## ORIGIN

Query Match	51.4%	Score	47.8	DB	5	Length	757
Best Local Similarity	5.8%	Pred.	No. 5	je-05			
Matches	49	Conservative	15	Mismatches	27	Indels	0
				Gaps			0
QY	2	CUGUUCGAAUCCAGCUGCAUGCUGUGUGUGUGUGAACCUGAACGUG	61				
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Db	210	CCTGTACGTAAATACGTTATGCATTAACCTGGGAACAATCTGAATCGATGAGAAG	269				
		: :					
QY	62	TTCAGTGCUGCUAAAAACGCCGAGGACGU	92				
		: :					

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Db 270 TAGATGGCTGCCGTAGAGAGCTGCAGATGT 300

Search completed: November 24, 2005, 01:30:28  
Job time : 1825 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:44:43 ; Search time 73.6667 Seconds  
(without alignments)  
2244.071 Million cell updates/sec

Title: US-09-475-158A-14

Perfect score: 1 gcguuuuccgaauccagcu.....guaaaaacugcagcgacgu 93

Scoring table: IDENTITY NUC  
Gapop 10'-0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Issued Patents, NA.\*  
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2: /cgn2\_6/ptodata/1/ina/5.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66.4	71.4	258	3	US-09-463-282D-26
2	63.8	68.6	141	2	US-08-468-275-3
3	63.8	68.6	141	2	US-08-468-275-5
4	63.8	68.6	141	3	US-09-007-466-3
5	63.8	68.6	141	3	US-09-007-466-5
6	63.8	68.6	141	3	US-08-952-980B-3
7	63.8	68.6	141	3	US-08-952-980B-5
8	63.8	68.6	207	2	US-08-142-551B-8
9	54.2	58.3	252	2	US-08-733-446-58
10	52.6	56.6	102	3	US-10-340-484-14
11	52.6	56.6	252	2	US-08-689-190-1
12	52.6	56.6	252	2	US-08-733-446-23
13	52.6	56.6	252	2	US-08-733-446-56
14	52.6	56.6	252	2	US-08-835-231-34
15	52.6	56.6	252	3	US-09-108-661-34
16	52.6	56.6	263	2	US-08-689-190-3
17	52.6	56.6	263	2	US-08-733-446-32
18	52.6	56.6	263	2	US-08-689-190-4
19	52.6	56.6	265	2	US-08-733-446-33
20	51	54.8	252	2	US-08-733-446-62
21	49.4	53.1	252	2	US-08-733-446-57
22	48.4	52.0	74	2	US-08-142-551B-132
23	47.8	51.4	252	2	US-07-863-014-1
24	47.8	51.4	252	2	US-08-332-453-1

25	47.8	51.4	537	2	US-08-835-231-5	Sequence 5, Appli
26	47.8	51.4	537	2	US-08-835-231-6	Sequence 6, Appli
27	47.8	51.4	537	3	US-09-108-661-5	Sequence 5, Appli
28	47.8	51.4	537	3	US-09-108-661-6	Sequence 6, Appli
29	47.8	51.4	601	3	US-09-949-016-18519	Sequence 18519, A
30	47.8	51.4	601	3	US-09-949-016-66782	Sequence 66782, A
31	47.8	51.4	772	3	US-09-949-016-51	Sequence 51, Appli
32	47.8	51.4	773	3	US-09-949-016-1970	Sequence 1970, Ap
33	47.8	51.4	7926	3	US-09-949-016-11793	Sequence 11793, A
34	47.8	51.4	7926	3	US-09-949-016-13712	Sequence 13712, A
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38	44.8	48.2	248	2	US-08-733-446-21	Sequence 21, Appli
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45	43	46.2	67	3	US-09-068-738A-9	Sequence 9, Appli

## ALIGNMENTS

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RESULT 1
US-09-463-282D-26
; Sequence 26, Application US/09463282D
; Patent No. 6500647
; GENERAL INFORMATION:
; APPLICANT: Jung, Eun-Kyung
; APPLICANT: Park, Doo-Hong
; APPLICANT: Chung, Soo Il
; TITLE OF INVENTION: RECOMBINANT EXPRESSION VECTOR OF HUMAN PARATHYROID HORMONE
; FILE REFERENCE: 0136/0656
; CURRENT APPLICATION NUMBER: US/09/463, 282D
; CURRENT FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: PCT/KR98/00146
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: KR 1997-35230
; PRIOR FILING DATE: 1997-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-463-282D-26

Query Match          71.4%; Score 66.4; DB 3; Length 258;
Best Local Similarity 59.8%; Pred. No. 2.5e-13;
Matches 55; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

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       62 TUGAUGGUGUGGUAUAAACUGCAGCAGCGUU 93
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DB      62 TTGAATGCTCGTAAATAACTGCAGATGTT 93
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RESULT 2
US-08-468-275-3
; Sequence 3, Application US/08468275
; Patent No. 5747453
; GENERAL INFORMATION:
; APPLICANT: HOLLADAY, LESLIE A.
; APPLICANT: OLDENBURG, KEVIN R.
; TITLE OF INVENTION: METHOD FOR INCREASING THE
; ELECTROTRANSFECT FLUX OF POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
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```

CORRESPONDENCE ADDRESS:
ADDRESSER: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,275
FILING DATE: 06-JUN-1995
CLASSIFICATION: 314
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
TELEPHONE: (415) 496-8150
TELEFAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 7..138
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 25
US-08-468-275-3
Query Match
Best Local Similarity 68.6%; Score 63.8; DB 2; Length 141;
Matches 56; Conservative 18; Mismatches 17; Indels 0; Gaps 0;
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QY 2 CUGUUCGGAUUCACUGAUGCAGGUGUGUGUGUGUCUGAACUCCAUAGGACUG 61
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Db 86 TTGAATGGCTCGTAAATAAACTGACGAGACGT 116
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RESULT 3
US-08-468-275-5/c
Sequence 5, Application US/08468275
Patent No. 5747453
GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,275
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
TELEPHONE: (415) 496-8150
TELEFAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-468-275-5
Query Match
Best Local Similarity 61.5%; Score 63.8; DB 2; Length 141;
Matches 56; Conservative 18; Mismatches 17; Indels 0; Gaps 0;
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QY 2 CUGUUCGGAUUCACUGAUGCAGGUGUGUGUGUGUCUGAACUCCAUAGGACUG 61
Db 116 CGGTTCCGAAATCCAGCTGCTGCACAACTGGGTAAACACTGAACCTCCTCGAGCGTG 57
QY 62 UUGAAUGGUGUGGUAUAAAAACUGCAGACGU 92
Db 56 TTGAATGGCTCGTAAATAAACTGACGAGACGT 26
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RESULT 4
US-09-007-466-3
Sequence 3, Application US/09007466
Patent No. 6313092
GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,466
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,275
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
TELEPHONE: (415) 496-8150
TELEFAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
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: STRAIDENESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (gen
:
: FEATURE:
:
: NAME/KEY: CDS
: LOCATION: 7..138
:
: FEATURE:
:
: NAME/KEY: mat_peptide
: LOCATION: 25
:
: US-09-007-466-3

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Query Match	68.6%	Score 63.8;	DB 3;	Length 141;
Best Local Similarity	61.5%;	Pred. No. 1.7e-12;		
Matches	56;	Conservative	18;	Mismatches 17;
				Indels 0;
				Gaps 0;

[illegible]

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1      RESULT 5
2      US-09-007-466-5/c
3      Sequence 5, Application US/0907466
4      Patent No. 6313092
5      GENERAL INFORMATION:
6      APPLICANT: HOLADAY, LESLIE A.
7      APPLICANT: OLDENBURG, KEVIN R.
8      TITLE OF INVENTION: METHOD FOR INCREASING THE
9      TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
10     NUMBER OF SEQUENCES: 10
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: ALZA CORPORATION
13     STREET: 950 PAGE MILL ROAD
14     CITY: PALO ALTO
15     STATE: CALIFORNIA
16     COUNTRY: USA
17     ZIP: 94303-0802
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: Floppy disk
20     COMPUTER: IBM PC compatible
21     OPERATING SYSTEM: PC-DOS/MS-DOS
22     SOFTWARE: Patent in Release #1.0, Version #1.30
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/09/007,466
25     FILING DATE:
26     CLASSIFICATION:
27     PRIOR APPLICATION DATA:
28     APPLICATION NUMBER: US 08/468,275
29     FILING DATE: 06-JUN-1995
30     ATTORNEY/AGENT INFORMATION:
31     NAME: MILLER, D. BYRON
32     REGISTRATION NUMBER: 30,661
33     REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
34     TELECOMMUNICATION INFORMATION:
35     TELEPHONE: (415) 496-8150
36     TELEFAX: (415) 496-8048
37     INFORMATION FOR SEQ ID NO: 5:
38     SEQUENCE CHARACTERISTICS:
39     LENGTH: 141 base pairs
40     TYPE: nucleic acid
41     STRANDEDNESS: single
42     TOPOLOGY: linear
43     MOLECULE TYPE: DNA (genomic)
44     US-09-007-466-5

```

Query Match	68.6%;	Score 63.8;	DB 3;	Length 141;
Best Local Similarity	61.5%;	Pred. No. 1.7e-12;		
Matches	56;	Conservative	18;	Mismatches 17;
				Indels 0;
				Gaps 0

[illegible]

```

1      RESULT 6
2      US-08-952-980B-3
3      Sequence 3, Application US/08952980B
4      Patent No. 633189
5      GENERAL INFORMATION:
6      APPLICANT: HOLLADAY, LESLIE A.
7      APPLICANT: KLEINBERG, KEVIN R.
8      TITLE OF INVENTION: METHOD FOR INCREASING THE
9      TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
10     NUMBER OF SEQUENCES: 12
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: ALZA CORPORATION
13     STREET: 950 PAGE MILL ROAD
14     CITY: PALO ALTO
15     STATE: CALIFORNIA
16     COUNTRY: USA
17     ZIP: 94303-0802
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: Floppy disk
20     COMPUTER: IBM PC compatible
21     OPERATING SYSTEM: PC-DOS/MS-DOS
22     SOFTWARE: Patent in Release #1.0, Version #1.30
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/08/952,980B
25     FILING DATE: 20-NOV-1997
26     CLASSIFICATION: 530
27     ATTORNEY/AGENT INFORMATION:
28     NAME: MILLER, D. BYRON
29     REGISTRATION NUMBER: 30,661
30     REFERENCE/DOCKET NUMBER: 2349 CIP 1
31     TELECOMMUNICATION INFORMATION:
32     TELEPHONE: (650) 496-8150
33     TELEFAX: (650) 496-8048
34     INFORMATION FOR SEQ ID NO: 3:
35     SEQUENCE CHARACTERISTICS:
36     LENGTH: 141 base pairs
37     TYPE: nucleic acid
38     STRANDEDNESS: single
39     TOPOLOGY: linear
40     MOLECULE TYPE: DNA (genomic)
41     FEATURE:
42     NAME/KEY: CDS
43     LOCATION: 7..138
44     FEATURE:
45     NAME/KEY: mat_peptide
46     LOCATION: 25
47     US-08-952-980B-3

```

Query Match	68.6%	Score 63.8;	DB 3;	Length 141;
Best Local Similarity	61.5%	Pred. No. 1.7e-12;		
Matches	56;	Conservative	18;	Mismatches 17;
			Indels	0;
			Gaps	0

QY 2 CTGTTCCGAAATCCACCTGCTGTCACAACTGGGTAAACACTGAACCTCCCTGACCGTG 85  
 Db 26 CCGTTTCGAAATCCACCTGCTGTCACAACTGGGTAAACACTGAACCTCCCTGACCGTG 85  
 QY 62 TTGATATGCTCTGTAAATAACTGACGACCT 116  
 Db 86 TTGATATGCTCTGTAAATAACTGACGACCT 116

RESULT 7  
US-08-952-980B-5/c  
; Sequence 5, Application US/08952980B



```

ADDRESS: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent'n Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,446
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/402,970
FILING DATE:
APPLICATION NUMBER: US/07/926,787
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NEUMER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 42025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..252
NAME/KEY: mutation
LOCATION: 19..24
IDENTIFICATION METHOD: E
US-08-733-446-58

Query Match          58.3%; Score 54.2; DB 2; Length 252;
Best Local Similarity 54.9%; Pred. No. 4e-09;
Matches 50; Conservative 18; Mismatches 23; Indels 0; Gaps 0;

QY      2 CUGUUUCCGAAAUCCAGCUGAUGCAGGUGUGUGUCUGAUCUCCAUUGAAGUG 61
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      2 CTGTGTCGAGATTCAGCTGCTGCTAATACCTTGCGCAACATTGGAATCTCATGGAGCGTG 61
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      62 UUGAUGGCGUCGUAUAAAACUGCAGACGU 92
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      62 TAGAATGGCTGCGTAAGAAAGTTGCAGAGATGT 92
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-10-340-484-14
Sequence 14, Application US/10340484
Patent No. 6875739
GENERAL INFORMATION:
APPLICANT: Stewart, Andrew F.
TITLE OF INVENTION: Treatment of Bone Disorders with Skeletal Anabolic
TITLE OF INVENTION: Drugs
FILE REFERENCE: 25200-501
CURRENT APPLICATION NUMBER: US/10/340,484
CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 60/347,215
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: 60/353,296
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 60/368,955

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PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/379,125
PRIOR FILING DATE: 2002-05-08
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patent'n Ver. 2.1
SEQ ID NO 14
LENGTH: 102
TYPE: DNA
ORGANISM: Homo sapiens
US-10-340-484-14

Query Match          56.6%; Score 52.6; DB 3; Length 102;
Best Local Similarity 53.8%; Pred. No. 1.1e-08;
Matches 49; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

QY      2 CUGUUUCCGAAAUCCAGCUGAUGCAGGUGUGUGUCUGAUCUCCAUUGAAGUG 61
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      2 CTGTGTCGAGATTCAGCTGCTGCTAATACCTTGCGCAACATTGGAATCTCATGGAGCGTG 61
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      62 UUGAUGGCGUCGUAUAAAACUGCAGACGU 92
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      62 TAGAATGGCTGCGTAAGAAAGTTGCAGAGATGT 92
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-08-689-190-1
Sequence 1, Application US/08689190
Patent No. 5714349
GENERAL INFORMATION:
APPLICANT: FUKUDA, Tsunehiko
APPLICANT: OSHIKA, Yuri
APPLICANT: YAMADA, Takao
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR HUMAN
TITLE OF INVENTION: PARATHYROID HORMONE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent'n Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,190
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/006,197
FILING DATE:
APPLICATION NUMBER: US/08/016,171
FILING DATE:
APPLICATION NUMBER: US/07/765,371
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, Gregory D
REGISTRATION NUMBER: 30,901
REFERENCE/DOCKET NUMBER: 41,288
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthesizing DNA

```



Query Match	56.6%;	Score 52.6;	DB 2;	Length 252;
Best Local Similarity	53.8%;	Pred. No. 1.4e-08;		

US-09-108-661-34

Fr1 Nov 25 10:36:36 2005

us-09-475-158a-14.rn1

Page 8

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Query Match: 56.6%; Score 52.6; DB 3; Length 252;
Best Local Similarity 53.8%; Pred. No. 1,4e-08;
Matches 49; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

QY      CUGUUNUCGAAUUCAGCUGAUGCUGUGUGUGUGUGUGUAACUUCGCAUGAACG 61
        :|::||::||::||::||::||::||::||::||::||::||::||::||:
Db       CUGTGTCCGAATTCAGTTATGCATAACTCGGCAACAATTGGAACTCATGAGCGTG 61

QY      UUGAUUGGCGUGUAAAAACUGCAGGACGU 92
        :|::||::||::||::||::||::||::||::||::||::||::||:
Db       TAGAATGCCCTGCTTAGAAGATTCGACGATGT 92

Search completed: November 24, 2005, 01:34:14
Job time : 74.6667 secs

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1  APPLICANT: Magner, F.
2  APPLICANT: Peng, L.
3  APPLICANT: Xia, U.
4  APPLICANT: Holmquist, B.
5  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptides
6  FILE REFERENCE: 1627,009US1
7  CURRENT APPLICATION NUMBER: US/10/997,700
8  CURRENT FILING DATE: 2004-11-24
9  PRIOR APPLICATION NUMBER: US 60/383,212
10 PRIOR FILING DATE: 2002-05-24
11 NUMBER OF SEQ ID NOS: 93
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 33
14 LENGTH: 102
15 TYPE: DNA
16 ORGANISM: Unknown
17 FEATURE:
18 OTHER INFORMATION: PTH (1-34) .
19 US-10-997-700-33

```

Query Match	74.8%	Score 69.6	DB 9	Length 102
Best Local Similarity	63.0%	Pred. No. 2.6e-15		
Matches	58	Conservative	20	Mismatches 14; Indels 0; Gaps 0;
QY	2	CUGUUCGGAU	UCCAGCUGGUGUGUGUGUUCUGAACUCCACUGAACGUG	61
Db	2	CTCTTCTTAAATCCAGCTGATGCACAACTGGGTAATACACTGAACCTATATGAAACG		61
QY	62	UUGAUGGCGUG	AAAAACUCGACGAGCGU	93
Db	62	TTGAATGCGCTGCTAAAAAAGCTGCAGGACGTT		93

RESULT 3  
US-10-997-078-61  
; Sequence 61, Application US/10997078  
; Publication No. US2005022144A1

```

APPLICANT: Peng, L.
APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
APPLICANT: Restoragen, Inc.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptides
FILE REFERENCE: 1637,010US1
CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16663
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 61
LENGTH: 111
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: PTH(1-37) .
US-10-997-078-61

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[illegible]

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RESULT 4
US-10-997-700-34
; Sequence 34, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, F.
; APPLICANT: Peng, L.
; APPLICANT: Xia, U.
; APPLICANT: Holmquist, B.
; TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptide
; FILE REFERENCE: 1627.009U51
; CURRENT APPLICATION NUMBER: US/10/997,700
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: US 60/363,212
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 111
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PTH(1-37).
US-10-997-700-34

```

[illegible]

RESULT 5  
US-10-997-078-141  
; Sequence 141, Application US/10997078

```

/ GENERAL INFORMATION:
/ APPLICANT: Wagner, F.
/ APPLICANT: Peng, L.
/ APPLICANT: Xia, U.
/ APPLICANT: Holmquist, B.
/ APPLICANT: Restoragen, Inc.
/ TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptides
/ FILE REFERENCE: 1627.010US1
/ CURRENT APPLICATION NUMBER: US/10/997, 078
/ CURRENT FILING DATE: 2004-11-24
/ PRIOR APPLICATION NUMBER: PCT/US03/16643
/ PRIOR FILING DATE: 2003-05-23
/ PRIOR APPLICATION NUMBER: US 60/383,370
/ PRIOR FILING DATE: 2002-05-24
/ NUMBER OF SEQ ID NOS: 148
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 141
/
/ LENGTH: 117
/
/ TYPE: DNA
/
/ ORGANISM: Artificial Sequence
/
/ FEATURE:
/
/ OTHER INFORMATION: A synthetic PTH sequence.
/
US-10-997-078-141

```

Query Match	74.8%	Score 69.6	DB 9	Length 117
Best Local Similarity	63.0%	Pred. No. 2,76-15		
Matches 58	Conservative 20	Mismatches 14	Indels 0	Gaps 0
QY	2	CUGUUCGGAUVCACAGUGAUGACGGUGUGUGUGUGU	CUGAACUCCAGUAGAAACGUG	61



Dd 2 CTGTTTCTGAATCAGCGTAGTCACAAACCCTGGSTAAACCACTCACTCATGGAACGTG 6

Qy 62 UUGAUAUGGCUCGCUAAAAAACUCCAGGACGUU 93  
:::|||||:::|||||||:::|||||:::  
Db 62 TTGAATGGCTCGTAAAAAACTCGCAGGACGTT 93

RESULT 6  
US-10-997-078-62  
; Sequence 62, Application US/10997078  
; Publication No. US2005022144A1

APPLICANT: magnet, E.  
 APPLICANT: peng, L.  
 APPLICANT: Xia, U.  
 APPLICANT: Holmquist, B.  
 APPLICANT: Restoragen, Inc.  
 TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptides

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```

; ORGANISM: Unknown  
 ;  
 ; FEATURE:  
 ;  
 ; OTHER INFORMATION: PTH(1-84),  
 ;  
 US-10-997-078-62

Query Match	74.8%;	Score 69.6;	DB 9;	Length 252;
Best Local Similarity	63.0%;	Pred. No. 3.3e-15;		
Matches	58;	Conservative	20;	Mismatches 14;
				Indels 0;
				Gaps 0

```
Qy      2 CUGUUTTCGAAAVCCAGCUCGUAGAUGCACGGUGUGUGGGUGGUCUGAACUCUCAAGGAACGUG    61
        |:|::|||:|||:|||:|||   |::|::|::|::|::|::|::|:
Db      2 CTGTTTCTGAATCCAGCTGATGCACAACCTGGGATAAACAACCTGAACCTTATGGAACGTG    61
```

```
Oy      62  UUGAUGGCGUCGUAUAAAAACUGCAGGACGU  93
      ::|||::|||::|||::|||::|||::
Db      62  TTGAATGGCTCGCTAAAAAACTGCAGGACGTT  93
```

RESULT 7  
US-10-997-700-35  
; Sequence 35, Application US/10997700  
; Publication No. US20050239172A1

```

; APPLICANT: Wagner, F.
; APPLICANT: Peng, L.
; APPLICANT: Xia, U.
; APPLICANT: Holmquist, B.
; TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptides

```

```

1 CURRENT APPLICATION NUMBER: US/10/997,700
2
3 CURRENT FILING DATE: 2004-11-24
4
5 PRIOR APPLICATION NUMBER: US 60/383,212
6
7 PRIOR FILING DATE: 2002-05-24
8
9 NUMBER OF SEQ ID NOS: 93
10
11 SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 35
; LENGTH: 252
;

```

**ORGANISM:** Unknown

OTHER INFORMATION: PTH(1-84)

US-10-997-700-35

Query Match	74.8%;	Score 69.6;	DB 9;	Length 252;
Best Local Similarity	63.0%;	Pred. No. 3.3e-15;		
Matches 58;	Conservative 20;	Mismatches 14;	Indels 0;	Gaps 0;

```

Oy      2  CUGUUUCCGAAAUCCAGCUCGUAUGCAGCGUGUGUGUGUGUCUCGAAUCUCCAUUGAAACGUG  61
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      2  CTGTTCTGTAATCAGCGTGAATGACACAACCTGGTAAACACCTGAACCTTAATGGAACGTG  61

```

```

QY      62  TUGAUGCUCUGCGUAAAAACUGCAGGACGU  93
        :::::::::::::
Db      62  TTGAATGGCTGCGTAAAAAAGTCAGGACGTT  93

```

US-10-997-700-89  
; Sequence 89, Application US/10997700  
; Publication No. US20050239172A1  
CENTRAL INFORMATION.

APPLICANT: Wagner, F.  
APPLICANT: Peng, I.

APPLICANT: Holmquist

TITLE OF INVENTION: MECHANISMS AND DNA CONSTRUCTS FOR HIGH ACID TOLERANCE OF *Escherichia coli*

CURRENT APPLICATION NUMBER: US/10/997,700

PRIOR APPLICATION NUMBER: US 60/383,212

NUMBER OF SEO ID NOS: 93

```

; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
;
; SEQ ID NO 89

```

LENGTH: 264

**ORGANISM:** Artificial Sequence

OTHER INFORMATION: A synthetic BEN121-M-PTH(1-84).

Query Match	74.8%	Score 69.6;	DB 9;	Length 264;
Best Local Similarity	63.0%;	Pred. No. 3.4e-15;		
Matches	58;	Conservative	20;	Mismatches 14;
			Indels	0;
			Gaps	0

DY  
DB

2 CUGUUUCCGAAAUCCAGCUGAUGCACCGUGUGUGUCGUCAUCCACUGGAACGUG 6  
|:::| |:::| |:::| |:| :||::| |:::| :::  
5 CTGTTCCTGAATCATCCACTGATGCACAACCCTGGSTAAAACACTGAACCTTATTGGAACGTG 6

**Dy** 62 UUGAUGCUCGCGUAAAAACUCAGGACGU 9  
::|||:|||:|||:|||:|||:|||::  
**Db** 65 TTGAATGGCTGCCGTAAAAAACTGCAGGACGT 9

RESULT 9  
US-10-997-762-18  
; Sequence 18, Application US/10997762  
; Publication No. US20050227313A1

; APPLICANT: Seo, Jin Seog  
 ; APPLICANT: Strydom, Daniel  
 ; APPLICANT: Holmquist, Barton  
 ; APPLICANT: Restoragen Inc.  
 ; TITLE OF INVENTION: Polypeptide Cleavage Processes

FILE REFERENCE: 162/.028051  
CURRENT APPLICATION NUMBER: US/10/997,762

PRIOR APPLICATION NUMBER: PCT/US03/16468

PRIOR APPLICATION NUMBER: US 60/383,488

NUMBER OF CEO ID NOS: 33

; SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 27

; TYPE: DNA

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of a chimeric synthetic protein
US-10-997-762-18

Query Match
Best Local Similarity 74.8%; Score 69.6; DB 9; Length 276;
Best Local Similarity 63.0%; Pred. No. 3,4e-15;
Matches 58; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 2 CUGUUCCGAAAUCCAGCUGAUGCAGUGUGUGUGUGUCUGAUCUCCAGUAAACGUG 61
DB 173 CTGTTCTGAAATCCAGCTGATGCAACAACCTGGTAAACACCTGAACCTATGGAACGTG 232
DB 233 TTGAATGGCTGCGTAAATAAAGCTGACAGACGTT 264

RESULT 10
US-10-997-822-3
; Sequence 3, Application US/10997822
; Publication No. US2005022731A1
; GENERAL INFORMATION:
; APPLICANT: Holmquist, B.
; APPLICANT: Strydom, D.
; APPLICANT: Genesalk, X.
; APPLICANT: Cyzer, R.
; TITLE OF INVENTION: POLYPEPTIDE CLEAVAGE PROCESS
; FILE REFERENCE: 1627.011US1
; CURRENT APPLICATION NUMBER: US/10/997,822
; PRIOR FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16647
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,484
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of a synthetic chimeric protein.
US-10-997-822-3

Query Match
Best Local Similarity 74.8%; Score 69.6; DB 9; Length 276;
Best Local Similarity 63.0%; Pred. No. 3,4e-15;
Matches 58; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 2 CUGUUCCGAAAUCCAGCUGAUGCAGUGUGUGUGUCUGAUCUCCAGUAAACGUG 61
DB 173 CTGTTCTGAAATCCAGCTGATGCAACAACCTGGTAAACACCTGAACCTATGGAACGTG 232
DB 233 TTGAATGGCTGCGTAAATAAAGCTGACAGACGTT 264

RESULT 11
US-10-997-700-75
; Sequence 75, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, F.
; APPLICANT: Peng, L.
; APPLICANT: Xia, U.
; APPLICANT: Holmquist, B.
; TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypept
; FILE REFERENCE: 1627.009US1
; CURRENT APPLICATION NUMBER: US/10/997,700
; PRIOR FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: US 60/383,212
; PRIOR FILING DATE: 2002-05-24
```

```

; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic PCR product.
US-10-997-700-75

Query Match
Best Local Similarity 74.8%; Score 69.6; DB 9; Length 276;
Best Local Similarity 63.0%; Pred. No. 3,4e-15;
Matches 58; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 2 CUGUUCCGAAAUCCAGCUGAUGCAGUGUGUGUGUCUGAUCUCCAGUAAACGUG 61
DB 14 CTGTTCTGAAATCCAGCTGATGCAACAACCTGGTAAACACCTGAACCTATGGAACGTG 73
DB 74 TTGAATGGCTGCGTAAATAAAGCTGACAGACGTT 105

RESULT 12
US-10-997-078-133
; Sequence 133, Application US/10997078
; Publication No. US2005022144A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, F.
; APPLICANT: Peng, L.
; APPLICANT: Xia, U.
; APPLICANT: Resstoregen, B.
; APPLICANT: Holmquist, B.
; TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypept
; FILE REFERENCE: 1627.010US1
; CURRENT APPLICATION NUMBER: US/10/997,078
; PRIOR FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16643
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,370
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic sequence for the T7cagVg-PTH(1-34) cassette.
US-10-997-078-133

Query Match
Best Local Similarity 74.8%; Score 69.6; DB 9; Length 282;
Best Local Similarity 63.0%; Pred. No. 3,4e-15;
Matches 58; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 2 CUGUUCCGAAAUCCAGCUGAUGCAGUGUGUGUGUCUGAUCUCCAGUAAACGUG 61
DB 167 CTGTTCTGAAATCCAGCTGATGCAACAACCTGGTAAACACCTGAACCTATGGAACGTG 226
DB 227 TTGAATGGCTGCGTAAATAAAGCTGACAGACGTT 258

RESULT 13
US-10-997-700-76
; Sequence 76, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, F.
; APPLICANT: Peng, L.
; APPLICANT: Xia, U.
; APPLICANT: Holmquist, B.
```

```

1  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptides
2  FILE REFERENCE: 1627 009US1
3  CURRENT APPLICATION NUMBER: US/10/997,700
4  CURRENT FILING DATE: 2004-11-24
5  PRIOR APPLICATION NUMBER: US 60/383,212
6  PRIOR FILING DATE: 2002-05-24
7  NUMBER OF SEQ ID NOS: 93
8  SOFTWARE: FASTSEQ for Windows Version 4.0
9  SEQ ID NO 76
10 LENGTH: 291
11 TYPE: DNA
12 ORGANISM: Artificial Sequence
13 FEATURE:
14 OTHER INFORMATION: A synthetic PCR product.
15 US-10-997-700-76

```

[illegible]

```

1      RESULT 14
2      US-10-997-700-77
3      ; Sequence 77, Application US/10997700
4      ; Publication No. US20050239172A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Wagner, F.
7      ; APPLICANT: Peng, L.
8      ; APPLICANT: Xia, U.
9      ; APPLICANT: Holmquist, B.
10     ; TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptides
11     ; FILE REFERENCE: 1627.0090S1
12     ; CURRENT APPLICATION NUMBER: US/10/997,700
13     ; CURRENT FILING DATE: 2004-11-24
14     ; PRIOR APPLICATION NUMBER: US 60/383,212
15     ; PRIOR FILING DATE: 2002-05-24
16     ; NUMBER OF SEQ ID NOS: 93
17     ; SOFTWARE: FastSeq for Windows Version 4.0
18     ; SEQ ID NO 77
19     ; LENGTH: 291
20     ; TYPE: DNA
21     ; ORGANISM: Artificial Sequence
22     ; FEATURE:
23     ; OTHER INFORMATION: A synthetic PCR product.
24     ; US-10-997-700-77

```

	74.8%	Score	69.6;	DB 9,	Length	291;
Query March	Similarity	63.0%;	Pred.	No. 3.4e-15;		
Best Local Match	Conservative	20;	Mismatches	14;	Indels	0; Gaps 0.
Oy	2 CUGUUUCGAAUVCACAGCGUGAUGCUGUGUCUAACAACCATVGGAACGGC	61				
Dd	29 CTGTTCGAAATCCAGCTGATGCACMACCTGGGTAAACACTTCACTCATGGAACGTG	88				
Oy	62 UUGAUUGCGUCGUAAAAAACUGCAGACGCU	93				
Dd	89 TTGAATGGCTGCTAAAATAAAGCTGCAAGAGCTTT	120				

RESULT 15  
US-10-997-700-91  
; Sequence 91, Application US/10997700  
; Publication No. US20050239172A1  
; GENERAL INFORMATION:  
; APPLICANT: Wagner, F.

```

? APPLICANT: Peng, L.
? APPLICANT: Xia, U.
? APPLICANT: Holmquist, B.
? TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
? FILE REFERENCE: 1697.009US1
? CURRENT APPLICATION NUMBER: US/10/997,700
? CURRENT FILING DATE: 2004-11-24
? PRIOR APPLICATION NUMBER: US 60/383,212
? PRIOR FILING DATE: 2002-05-24
? NUMBER OF SEQ ID NOS: 93
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 91
? LENGTH: 321
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: A synthetic pBN121-T7tag-CH-PTH(1-84).
US-10-997-700-91

```

[illegible]

Search completed: November 24, 2005, 04:46:55  
Job time : 412.667 secs

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```

? APPLICANT: Labat, Ivan
? APPLICANT: Stache-Crain, Birgit
? APPLICANT: Andarmani, Susan
? APPLICANT: Tang, Y. Tom
? TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
? FILE REFERENCE: 821A
? CURRENT APPLICATION NUMBER: US/10/821,234
? CURRENT FILING DATE: 2004-04-07
? PRIOR APPLICATION NUMBER: US 60/462,047
? PRIOR FILING DATE: 2003-04-07
? NUMBER OF SEQ ID NOS: 1704
? SOFTWARE: pc_seq_genes Version 1.0
? SEQ ID NO 760
? LENGTH: 2327
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-10-821-234-760

```

Query Match	27.1%	Score 25.2	DB 1	Length 2227
Best Local Similarity	43.6%	Ped. No. 3		
Matches	33	Conservative	11	Mismatches 33; Indels 0; Gaps 0;
QY	16	CACGCAUAGCAGCGUGUGUGUGUTGAAUCCAGGAGAGUGUGUAAGUGUGCU	75	
DB	894	CACCTCTCTGCCCTGGGTGGTGGAGGCGGTACCGCTACACACATATGTGGCAITGGT	835	
	76	AAAAAACUGCAGGAGCUU	93	
QY		.....:::		
DB	834	GAGGATCTGCTGCAGGTT	817	

```

RESULT 3
US-10-526-731-4
; Sequence 4, Application US/10526731
; Publication No. US2005024437A1
; GENERAL INFORMATION:
; APPLICANT: AKZO Nobel N.V.
; TITLE OF INVENTION: Live attenuated parasite vaccine
; FILE REFERENCE: 2002-017-EP
; CURRENT APPLICATION NUMBER: US/10/526,731
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: EP 02078953
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Toxoplasma gondii
US-10-526-731-4

```

Query Match: 25.8%; Score 24; DB 1; Length 2748;  
Best Local Similarity 54.2%; Pzed No. 9.3;  
Matches 22; Conservative 7; Mismatches 15; Indels 0; Gaps 0

RESULT 4  
 US-11-164-005-23/c  
 : Sequence 23, Application US/11184005  
 : Publication No. US20050256052A1  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Luyten, Frank P.  
 : APPLICANT: Moos, Malcolm Jr.  
 :  
 : APPLICANT: Wang, Bang  
 : APPLICANT: Wang, Bang  
 :  
 : TITLE OF INVENTION: METHOD OF MODULATING TISSUE  
 : TITLE OF INVENTION: GROWTH USING F2BZ PROTEIN  
 : FILE REFERENCE: NIH33.1CFC3  
 : CURRENT APPLICATION NUMBER: US/11/164, 005

```

? CURRENT FILING DATE: 2005-07-18
? PRIOR APPLICATION NUMBER: US 10/028051
? PRIOR FILING DATE: 2001-12-19
? PRIOR APPLICATION NUMBER: US 08/822333
? PRIOR FILING DATE: 1997-03-20
? PRIOR APPLICATION NUMBER: US 08/729,452
? PRIOR FILING DATE: 1996-10-11
? NUMBER OF SEQ ID NOS: 23
? SOFTWARE: FastSeq for Windows Version 4.0.
? SEQ ID NO 23
? LENGTH: 1291
? TYPE: DNA
? ORGANISM: Xenopus laevis
? US-11-184-005-23

```

[illegible]

```

RESULT 5 -
US-10-131-826A-351
: Sequence 351, Application US/10/131826A
: Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvarolt, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zhenlin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACTIS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131, 826A
CURRENT FILING DATE: 2002-04-24
PRIORITY APPLICATION NUMBER: 60/049911
PRIORITY FILING DATE: 1997-06-18
PRIORITY APPLICATION NUMBER: 60/056974
PRIORITY FILING DATE: 1997-08-26
PRIORITY APPLICATION NUMBER: 60/059113
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059115
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059117
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059122
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059184
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059263
PRIORITY FILING DATE: 1997-09-18
PRIORITY APPLICATION NUMBER: 60/059352
PRIORITY FILING DATE: 1997-09-19

```



```
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberbauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPN
; CURRENT APPLICATION NUMBER: US/11/082,389
; PRIOR FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 315
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1438)
; OTHER INFORMATION: KXN01995
; US-11-082-389-315

Query Match      23.9%; Score 22.2; DB 9; Length 1461;
Best Local Similarity 45.1%; Pred. No. 35;
Matches 23; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY      4  GUUUCGAAUCCAGCUGAUCACGAGUGUGUGUGUGUGUGAUCUCCG 54
Db      1148 GTTGCTGGCGGCGATCATGATGATGCTGCTGTCTGTACACCTGTG 1198

RESULT 10
; US-11-074-176-353
; Sequence 353, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAniff, Olivia
; APPLICANT: Perill, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 353
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1209)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: ORF 699; phosphoglycerate kinase
; US-11-074-176-353

Query Match      23.4%; Score 21.8; DB 7; Length 1209;
Best Local Similarity 44.9%; Pred. No. 46;
Matches 22; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY      28  GGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUG 76
Db      1141 GGTGGTGGTGGTCTTCACTTACTTACTTGAAGTAAGTATTCGACGTA 1189

RESULT 11
; US-11-074-176-185
; Sequence 185, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAniff, Olivia
; APPLICANT: Perill, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185
; LENGTH: 1224
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1224)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: ORF 699; phosphoglycerate kinase
; US-11-074-176-185

Query Match      23.4%; Score 21.8; DB 7; Length 1224;
Best Local Similarity 44.9%; Pred. No. 46;
Matches 22; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY      28  GGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUG 76
Db      1156 GGTGGTGGTGGTCTTCACTTACTTACTTGAAGTAAGTATTCGACGTA 1204

RESULT 12
; US-10-793-626-4301/C
; Sequence 4301, Application US/10793626
; Publication No. US20050253478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUJ480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
```



```

? PRIOR APPLICATION NUMBER: 60/164,258
? PRIOR FILING DATE: 1999-11-09
? NUMBER OF SEQ. ID NOS.: 4472
? SOFTWARE: PatentIn Ver. 2.1
? SEQ. ID NO. 4301
? LENGTH: 2536
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-4301

```

	Query Match	23.4%	Score 21.8;	DB 1;	length 2536;
	Best Local Similarity	44.9%;	Pred. No. 56;		
	Matches	22;	Conservative	10;	Mismatches 17; Indels 0; Gaps 0;
Oy	33	ucgucugcugcugaacuccagcaacgcugucgaatggccguataaaaa	81		
Db	1705	tgcgttttgcttctactccaaagaagaaatgacactgcatgtataggaaa	1657		

```

RESULT 13
US-10-821-234-748/C
, Sequence 748, Application US/10621234
, Publication No. US200502551141
, GENERAL INFORMATION:
, APPLICANT: Labat, Ivan
, APPLICANT: Stache-Crain, Birgit
, APPLICANT: Andarmani, Susan
, APPLICANT: Tang, Y. Tom
, TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
, FILE REFERENCE: 821A
, CURRENT APPLICATION NUMBER: US/10/821,234
, CURRENT FILING DATE: 2004-04-07
, PRIOR APPLICATION NUMBER: US 60/462,047
, PRIOR FILING DATE: 2003-04-07
, NUMBER OF SEQ ID NOS: 1704
, SOFTWARE: pt_seq_genes Version 1.0
, SEQ ID NO 748
, LENGTH: 1759
, TYPE: DNA
, ORGANISM: Homo sapiens
US-10-821-234-748

```

	Query Match	23.2%	Score 21.6;	DB 1;	Length 1759;	
	Best Local Similarity	44.1%;	Pred. No. 60;			
	Matches	30;	Conservative	9;	Mismatches 29;	Indels 0; Gaps 0
QY	7 UCCGAAUCCACUUAUGCAGCGUGUGUGUGUGUCUACAUCUCAAGCAAGUGUGAA	66				
	: :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :					
Dd	469 TTCGGTAGGCTCTCTGCAGCGACCAGTACTGCTGTGAACCTTCAGTGCGTTTGAA	410				
QY	67 UGCGUGCG	74				
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :					
Dd	409 ATCTCTGCG	402				

```

RESULT 14
US-10-821-234-112
; Sequence 112, Application US/10821234
; Publication No. US20050255114v1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andermani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07

```

```

; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 112
; LENGTH: 3901
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-112

```

[illegible]

```

RESULT 15
US-10-821-234-598
; Sequence 598, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 598
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-598

```

```

Query Match      22.8%; Score 21.2; DB 1; Length 459;
Best Local Similarity 50.0%; Pred. No. 58;
Matches 29; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY      14 UCCAGCUAUACACGCGUGUGUGUGUCUGAAUCUCCAUUGAAUGUGUAUGUCU 71
      |||||:|||||:|||||:|||||:|||||:
Db       17 TCCTGCTAAGCCCTGCTGCGGAGGAGGCACAGAGCGAGATGGGGCGTATGGATGCT 74

```

Search completed: November 24, 2005, 04:56:47  
Job time : 195 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:00:32 ; Search time 242.667 Seconds  
(without alignments)  
2554.189 Million cell updates/sec

Title: US-09-475-158A-15

Perfect score: 1 gcguuuuccgaauccagcu.....guaaaaacugcaggacguu 93

Sequence: 1 gcguuuuccgaauccagcu.....guaaaaacugcaggacguu 93

Scoring table: IDENTITY NUC  
Gapop 10-0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: N\_Geneseq\_21:\*

1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	93	100.0	93	3	AAAS1730	AAAS1730 PTH funct
2	83.4	89.7	93	3	AAAS1729	AAAS1729 PTH funct
3	64.2	69.0	93	3	AAAS1731	AAAS1731 PTH funct
4	61.6	66.2	152	2	AAAT73910	AAAT73910 Synthetic
5	60	64.5	102	12	ADG93179	ADG93179 Novel exp
6	60	64.5	102	12	ADJ65857	ADJ65857 PTH pepti
7	60	64.5	102	13	ADW14377	ADW14377 Human par
8	60	64.5	111	12	ADG93180	ADG93180 Novel exp
9	60	64.5	111	12	ADJ65858	ADJ65858 PTH pepti
10	60	64.5	111	13	ADM14375	ADM14375 Human par
11	60	64.5	117	12	ADG93260	ADG93260 Novel exp
12	60	64.5	168	2	AAAT34865	AAAT34865 Plasmid p
13	60	64.5	252	12	ADG93181	ADG93181 Novel exp
14	60	64.5	252	12	ADJ65859	ADJ65859 PTH prote
15	60	64.5	264	12	ADJ65913	ADJ65913 Tandem po
16	60	64.5	276	12	ADFP90345	ADFP90345 Chimeric
17	60	64.5	276	12	ADJ65899	ADJ65899 PTH DNA s
18	60	64.5	276	12	ADJ87051	ADJ87051 Nucleotid
19	60	64.5	282	12	ADG93252	ADG93252 Novel exp

20	60	64.5	291	12	ADJ65901	ADJ65901 PTH DNA s
21	60	64.5	291	12	ADJ65900	ADJ65900 PTH DNA s
22	60	64.5	294	12	AAAT34866	AAAT34866 Plasmid p
23	60	64.5	321	12	ADJ65915	ADJ65915 Tandem po
24	60	64.5	420	12	ADJ65917	ADJ65917 Tandem po
25	60	64.5	426	12	ADFP90347	ADFP90347 Chimeric
26	60	64.5	528	6	AAAT19702	AAAT19702 DNA encod
27	58.4	62.8	108	13	ADJ69494	ADJ69494 Human par
28	58.4	62.8	114	13	ADJ69502	ADJ69502 Human par
29	58.4	62.8	489	12	ADG48030	ADG48030 Human PTH
30	58.4	62.8	489	12	ADG48059	ADG48059 Human PTH
31	58.4	62.8	489	12	ADG68786	ADG68786 Human mut
32	54.2	58.3	141	2	AAO89920	AAO89920 Recombina
33	54.2	58.3	141	2	AAAT80383	AAAT80383 rPTH codi
34	54.2	58.3	207	2	AAO89923	AAO89923 Expressio
35	52.6	56.6	145	13	ADW80822	ADW80822 DNA encod
36	51	54.8	728	2	AAO55301	AAO55301 Truncated
37	51	54.8	945	2	AAO55302	AAO55302 gp55-Abn-
38	50.4	54.2	405	3	AAAS1452	AAAS1452 PCPB-RVR-
39	50.4	54.2	408	3	AAAS1455	AAAS1455 PCPB-LVPR
40	50.4	54.2	408	3	AAAS1454	AAAS1454 PCPB-TEGR
41	50.4	54.2	411	3	AAAS1453	AAAS1453 PCPB-ALY-
42	50.4	54.2	414	3	AAAS1459	AAAS1459 PCPB-APR-
43	50.4	54.2	417	3	AAAS1456	AAAS1456 PCPB-VIPR
44	50.4	54.2	423	3	AAAS1457	AAAS1457 PCPB-DQVD
45	50.4	54.2	435	3	AAAS1458	AAAS1458 PCPB-DEFA

## ALIGNMENTS

RESULT 1  
ID AAAS1730 standard; RNA; 93 BP.

XX AAAS1730;

DT 31-OCT-2000 (first entry)

XX PTH functional domain conjugate peptide PG7 coding sequence.

XX PTH: parathyroid hormone; conjugate; bone mass; bone reformation;

KM resorption; remodeling; tether1; osteoporosis; ss.

XX Homo sapiens.

OS Synthetic.

XX Location/Qualifiers

FT Key 1..93

FT CDS /\*tag= a

FT product= "PG7"

XX MO200039278-A2.

PD 06-JUL-2000.

XX 30-DEC-1999; 99WO-US031108.

XX 31-DEC-1998; 98US-0114577P.

XX (GARD/) GARDELLA T J.

XX (KRON/) KRONENBERG H M.

XX (POT/) POTTS J T.

XX (JUEP/) JUEPPNER H.

XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

DR WPI: 2000-452384/39.

XX P-PSDB; AAY96975.

PT New compound comprising an amino terminal signaling functional domain

PT linked to a carboxy-terminal binding portion of parathyroid hormone for

PT treating mammalian conditions characterized by decreases in bone mass.

XX Claim 14; Fig 1; 119pp; English.

PS

CC Compound of the structure or formula S-(L)-n-B, R1-S-(L)-n-R or S-(L)-n  
XX -R, are new. S is an amino terminal signaling functional domain of  
CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
CC portion of PTH(1-34) or a PTH-related protein (PTHrP) (1-34); R1 is the  
CC PTH-1 receptor signal sequence; and R is a portion of PTH-1 receptor  
CC sequence. The new compounds are used for treating mammalian conditions  
CC characterized by decreases in bone mass, determining rates of bone  
CC reformation, bone resorption and/or bone remodeling, treating diseases  
CC and disorders associated with decreased tethered activity, increasing cAMP  
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
CC non-peptide PTH (claimed). The new compound can be administered by  
CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
CC regular injections to treat osteoporosis

XX

SQ Sequence 93 BP; 19 A; 16 C; 33 G; 0 T; 25 U; 0 Other;

Query Match 100.0%; Score 93; DB 3; Length 93;  
Best Local Similarity 100.0%; Pred. No. 3,7e-20;  
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 1 GCUGUUYCCGAANAUCAGCUGAUGCACGUGUGUGUGUGUGUCCAGAAACGU 60  
Db 1 GCUGUUYCCGAANAUCAGCUGAUGCACGUGUGUGUGUGUGUCCAGAAACGU 60  
|||||  
OY 61 GUUGAAGCGUGCGUUAAAAAACUGCAGACCGU 93  
Db 61 GUUGAAGCGUGCGUUAAAAAACUGCAGACCGU 93  
|||||

RESULT 2  
AAA51729  
ID AAA51729 standard; RNA; 93 BP.  
XX  
AC AAA51729;  
DT 31-OCT-2000 (first entry)  
XX  
DE PTH functional domain conjugate peptide PG5 coding sequence.  
XX  
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;  
XX resorption; remodeling; tether1; osteoporosis; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..93  
FT /\*tag= a  
FT /product= "PG5"  
XX  
XX MO200039278-A2.  
XX  
PD 06-JUL-2000.  
XX  
PE 30-DEC-1999; 99WO-US031108.  
XX  
PR 31-DEC-1998; 98US-0114577P.  
XX  
PA ((KRON//) GARDELIA T J,  
PA (KRON//) KRONENBERG H M,  
PA (POT//) POTTS JT,  
PA (JUEP//) JUEPPNER H.  
XX  
PI Gardeila TJ, Kronenberg HM, Potts JT, Jueppner H;  
XX WPI; 2000-452384/39.  
DR  
OR P-PSDB; AA936973.  
XX  
XX New compound comprising an amino terminal signaling functional domain

**Claim 14; Fig 1; 119pp; English.**

Compounds of the structure or formula S-(L)<sub>n</sub>-B, R<sub>1</sub>S-(L)<sub>n</sub>-R or S-(L)<sub>n</sub>-R are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTHrP) (1-34); R<sub>1</sub> is the PTH-1 receptor signal sequence; and R is a portion of PTH-1 receptor characterized by decreases in bone mass, remodeling rates of bone reformation, bone resorption and/or bone remodeling treating diseases and disorders associated with decreased telnet activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by intramuscular injection like the large native PTH or PTHrP which avoids the need for regular injections to treat osteoporosis

Sequence 93 BP; 21 A; 18 C; 30 G; 0 T; 24 U; 0 Other;

Query Match	89.7%; Score 83.4; DB 3;	Length 93;
Best Local Similarity	93.5%;	Pred.No. 4,6e-17;
Matches	87; Conservative	0; Mismatches 6; Indels 0; Gaps 0

```
Oy      1 GCUGUUYCCGAAAUUCAGCUGCAGCGUGUGUGUGUGUGUGUGUGUCCAUUGAACGU    60
Db      1 GCUGUUYYCCGAUAUUCAGCUGCAGCGUGUGUGUGUGUGUGUGUCCAUCGAAACGU    60
Oy          |||||
Db          |||||
Oy      61 GUUGAUVGGCUCGUAATAAAAACUCGACGACCGUU    93
Db      61 GUUGAUVGGCUCGUAAAAAAAACUCGACGACCGUU    93
```

RESULT 3  
ID AAAS1731 standard; RNA; 93 BP.  
AAAS1731:  
  
DT 31-OCT-2000 (first entry)

PTH functional domain conjugate peptide PG9 coding sequence.

DZ PTH; parathyroid hormone; conjugate; bone mass; bone reformation;  
KW resorption; remodeling; tether; osteoporois; ss.  
XX Homo sapiens.  
OS Synthetic.

Key	Location/Qualifiers
FT CDS	1..93
FT FT	/tag= a
FT FT	/product= "PG9"

WO200039278-A2.

PD 06-JUL-2000.

PF 30-DEC-1999; 99MO-US031108.

PR 31-DEC-1998; 98US-0114577P.

PA (GARDEL/) GARDEILA T J.  
PA (KRONENBERG H M.) KRONENBERG H M.  
PA (POTTS JT) POTTS JT.  
PA (JUEPPNER H) JUEPPNER H.

PI Gardeila TJ, Kronenberg HM, Potts JT, Jueppner H;  
WI PI: 2000-452384/39.  
DR P-PDSDB; AAY96974.

XX New compound comprising an amino terminal signaling functional domain  
PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
PT treating mammalian conditions characterized by decreases in bone mass.  
XX  
PS Claim 14, Fig 1, 11pp; English.

CC Compounds of the structure or formula S-(L), n-B-R, 1-S-(L), n-R or S-(L) -  
CC -R, are new. S is an amino terminal signaling functional domain of  
CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R is the  
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
CC sequence. The new compounds are used for treating mammalian conditions  
CC characterized by decreases in bone mass, determining rates of bone  
CC reformation, bone resorption and/or bone remodeling, treating diseases  
CC and disorders associated with decreased tethari activity, increasing cAMP  
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
CC non-peptide PTH (claimed). The new compound can be administered by  
CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
CC regular injections to treat osteoporosis

**SQ** Sequence 93 BP; 18 A; 14 C; 35 G; 0 T; 26 U; 0 Other;

Query Match	69.0%	Score 64.2	DB 3	length 93
Best Local Similarity	80.6%	Pred. No. 7e-11		
Matches 75, Conservative		0	Mismatches 18,	Indels 0; Gaps 0;

[illegible]

Qy 61 GUTGAUUGGCGUAAAAAACUGCAGCAGCGUU 93  
|||  
Db 61 GUTGAUUGGCGUAAAAAACUGCAGCAGCGUU 93

RESULT 4  
AAT73910  
ID AAT73910 standard; DNA; 152 BP.

AC AAT73910;

DT	25-MAR-2003	(revised)
DT	30-JAN-1998	(first entry)

DE Synthetic oligonucleotide encoding linker and PTH 1-37.

KM Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin; fusion protein.  
 KW recombinant production; endoproteinase LysC; ds.

OS Synthetic.  
OS Homo sapiens.

	Key	Location/Qualifiers
FH	misc_feature	1. . 4
FT		/44

```

FT      /label= sticky end
FT      /note= "5' end of complementary strand overhangs 3' end
FT      of present strand by sequence 5'-TCGA-3'"
FT      6..152
CDS
FT      /*tag= a

```

PN WO9718314-A1.

PD 22-MAY-1997

PF 06-NOV-1996; 96WO-EP004850.

PR 16-NOV-1995; 95DE-01042702.

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

XX

PI Kopecki E;

DR WPI; 1997-289290/26.  
DR P-PSDB; AAW21946.

PT Recombinant production of peptide(s) as fusions with streptavidin  
PT attached via cleavable linker - especially for urotropin and parathyroid  
PT hormone production.

PS Example 2; Fig 2; 37pp; German.

The present sequence, which encodes a linker and the parathyroid hormone 1-37 (PTH 1-37) peptide with codon usage optimised for *E. coli*, was ligated to the 2.9 kb *NheI*-*HindIII* fragment of pSAM-CORE, which contains the Met (13-139) secretaphilin (SA) sequence, to give pSA-EK-PTH. pSA-EK-PTH and the LacIq repressor plasmid pUBS500 were used to transform *E. coli* K12 RM82. The transformants were grown, with IPTG induction, in medium containing kanamycin and ampicillin. Cells were harvested, lysed and isolated inclusion bodies solubilised in guanidine hydrochloride, and renatured by dilution in pH 7 phosphate buffer. The solution was clarified and the supernatant concentrated and purified on a column of immobilised iminobiotin. The purified material was incubated with endoprotease LysC and the PTH 1-37 fragment released, recovered by SA fragment removal on an iminobiotin column followed by chromatography on a Fractogel and reverse phase HPLC. The endoprotease LysC cleaves the fusion protein rapidly and completely, exclusively at the Lys residue in the linker, 1.e. not at Lys residues in SA. (updated on 25-MAR-2003 to correct PR field.)

**5Q** Sequence 152 BP; 44 A; 38 C; 35 G; 35 T; 0 U; 0 Other;

Query Match	66.2%	Score 61.6	DB 2	Length 152
Best Local Similarity	59.8%	Pred. NC. 5.4e-10		
Matches 55, Conservative	18	Mismatches 13	Indels 0	Gaps 0

```
Ox      2 CUGUUUCCGAUAUCCAGCTGATGCACCGSUGUGUGUCGUGUGGUCCAUGAAACGUG   61
           |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     37 CCGTTTCCGAATTCAAGCTGATGCACAACCTGGTAACACTCATTGAAACGTG   96
```

Oy      62 UGCAUUGGCUCGCCUA AAAAACUCAGACGU 93  
         ::| | : | | : | | : | | : | | :  
Db     97 TTGAATGGCTCGTAA AAAAACTCAGACGT 128

RESULT 5	
ADG93179	
ID	ADG93179 standard; DNA; 102 BP.

AC ADG93179;

DT 11-MAR-2004 (first entry)

DE Novel expression cassette-related polypeptide-encoding DNA Seqid60.

KW expression cassette; high yield polypeptide production,  
tandem polypeptide; inclusion body; gene; ds.

OS Unidentified.

PN WO2003100021-A2

PD 04-DEC-2003.

PF 23-MAY-2003; 2003WO-US016643

PR 24-MAY-2002; 2002US-0383370P

PA (REST-) RESTORAGEN INC.

[illegible]

XX 0004 03E126/03  
25

DRE

DR P-PSDB; ADG93159.  
XX New expression cassette comprising an operably linked nucleic acid  
PT sequence, useful for producing a tandem polypeptide that forms an  
PT inclusion body when expressed in a cell.  
XX  
XX  
PS Disclosure; SEQ ID NO 60; 157pp; English.  
XX This invention relates to a novel expression cassette and methods for  
CC high yield production of polypeptides. The cassette comprises an operably  
CC linked nucleic acid sequence, where the expression of the cassette  
CC produces a tandem polypeptide that forms an inclusion body when expressed  
CC in a cell. The expression cassette is useful for producing peptide and  
CC polypeptide in a cell, preferably a tandem polypeptide that forms an  
CC inclusion body when expressed in a cell. The present sequence is that of  
CC the expression cassette of the invention.  
XX  
SQ Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;  
Query Match 64.5%; Score 60; DB 12; Length 102;  
Best Local Similarity 57.6%; Pred. No. 1.6e-09;  
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;  
QY 2 CUGUUCGGAUAUCCAGCUGAUGCAGUGUGUGUGUGUGUGUCCAUUGAAGCUG 61  
DB 2 CTGTTCTGAATCTCAGCTGATGCACACCTGGTAACACCTGAACCTATGAGACGTG 61  
QY 62 UUGAUGGCGUGCGUAAAAAACUGCAGACGCU 93  
DB 62 TTGAATGCTGCGTAAAAAACTGCAGACGTT 93  
RESULT 6  
ADJ65857  
ID ADJ65857 standard; DNA; 102 BP.  
XX  
XX ADJ65857;  
AC  
XX  
XX 06-MAY-2004 (first entry)  
PT  
XX  
XX PTH peptide coding sequence #1.  
DE  
XX  
XX expression cassette; tandem polypeptide; inclusion body;  
KM inclusion body fusion partner; PTH; gene; ds.  
XX  
XX Unidentified.  
OS  
XX  
XX WO2003100022-A2.  
PN  
XX  
XX 04-DEC-2003.  
PD  
XX  
XX 23-MAY-2003; 2003WO-US016645.  
PF  
XX  
XX 24-MAY-2002; 2002US-0383212P.  
PR  
XX  
XX (REST-) RESTORAGEN INC.  
PA  
XX  
XX Xia Y, Peng L;  
PI  
XX  
XX WPI; 2004-035129/03.  
DR  
XX  
XX P-PSDB; ADJ65837.  
PT  
XX  
XX New expression cassette comprising an operably linked nucleic acid  
PT sequence, useful for producing a tandem polypeptide that forms an  
PT inclusion body when expressed in a cell.  
XX  
XX  
XX Disclosure; SEQ ID NO 33; 132pp; English.  
XX The invention comprises an expression cassette which produces a tandem  
CC polypeptide that form an inclusion body when expressed in a cell. The  
CC expression cassette of the invention is useful for producing a peptide or  
CC polypeptide in a cell, preferably a tandem polypeptide that forms an

CC inclusion body when expressed in a cell. The present DNA sequence encodes  
CC a peptide which may be used in the construction of a tandem polypeptide  
CC of the invention.  
XX  
XX  
SQ Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;  
Query Match 64.5%; Score 60; DB 12; Length 102;  
Best Local Similarity 57.6%; Pred. No. 1.6e-09;  
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;  
QY 2 CUGUUCGGAUAUCCAGCUGAUGCAGUGUGUGUGUGUGUCCAUUGAAGCUG 61  
DB 2 CTGTTCTGAATCTCAGCTGATGCACACCTGGTAACACCTGAACCTATGAGACGTG 61  
QY 62 UUGAUGGCGUGCGUAAAAAACUGCAGACGCU 93  
DB 62 TTGAATGCTGCGTAAAAAACTGCAGACGTT 93  
RESULT 7  
ADM14377  
ID ADM14377 standard; DNA; 102 BP.  
XX  
XX ADM14377;  
AC  
XX  
XX 10-MAR-2005 (first entry)  
PT  
XX  
XX Human parathyroxin PTH 1-34 peptide encoding DNA SEQ ID NO:3.  
DE  
XX  
XX ds; parathyroxin; recombinant protein; protein engineering.  
KM  
XX  
XX Homo sapiens.  
OS  
XX  
XX CN1424325-A.  
PN  
XX  
XX 18-JUN-2003.  
PD  
XX  
XX 12-DEC-2001; 2001CN-00142627.  
PF  
XX  
XX 12-DEC-2001; 2001CN-00142627.  
PR  
XX  
XX (SHAN-) SHANGHAI BIOLOGICAL ENG RES CENT ACAD S.  
XX  
XX  
XX Chen C, Xiu C, Li M;  
PI  
XX  
XX WPI; 2004-099606/11.  
DR  
XX  
XX P-PSDB; ADM14378.  
PT  
XX  
XX Production of reorganized human parathyroid hormone 1-34 peptide.  
PT  
XX  
XX Disclosure; SEQ ID NO 3; 25pp; Chinese.  
PS  
XX  
XX The invention relates to a novel process for preparing recombinant human  
CC parathyroxin 1-34 peptide, including such steps as culturing a host cell  
CC in proper conditions, separating G1y-Ser-Pro-PTH 1-34 peptide (ADM14376),  
CC severing by Pro endopeptidase to form PTH 1-34 peptide (ADM14378) and  
CC separating and purifying PTH 1-34 peptide. The present sequence encodes  
CC the PTH 1-34 peptide.  
XX  
XX  
SQ Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;  
Query Match 64.5%; Score 60; DB 13; Length 102;  
Best Local Similarity 57.6%; Pred. No. 1.6e-09;  
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;  
QY 2 CUGUUCGGAUAUCCAGCUGAUGCAGUGUGUGUGUGUGUCCAUUGAAGCUG 61  
DB 2 CTGTTCTGAATCTCAGCTGATGCACACCTGGTAACACCTGAACCTATGAGACGTG 61  
QY 62 UUGAUGGCGUGCGUAAAAAACUGCAGACGCU 93  
DB 62 TTGAATGCTGCGTAAAAAACTGCAGACGTT 93

## RESULT 8

ADG93180

ID ADG93180 standard; DNA; 111 BP.

XX ADG93180;

XX 11-MAR-2004 (first entry)

XX Novel expression cassette-related polypeptide-encoding DNA seqID61.

XX expression cassette; high yield polypeptide production;

XX tandem polypeptide; inclusion body; gene; ds.

XX Unidentified.

XX WO2003100021-A2.

XX 04-DEC-2003.

XX 23-MAY-2003; 2003WO-US016643.

XX 24-MAY-2002; 2002US-0383370P.

XX (REST-) RESTORAGEN INC.

XX (HARL/) HARLEY S.

XX Harley S, Williams JA, Luan P, Xia Y;

XX WPI; 2004-035128/03.

XX P-PSDB; ADG93160.

XX New expression cassette comprising an operably linked nucleic acid

XX sequence, useful for producing a tandem polypeptide that forms an

XX inclusion body when expressed in a cell.

XX Disclosure; SEQ ID NO 61; 157pp; English.

XX This invention relates to a novel expression cassette and methods for

XX high yield production of polypeptides. The cassette comprises an operably

XX linked nucleic acid sequence, where the expression of the cassette

XX produces a tandem polypeptide that forms an inclusion body when expressed

XX in a cell. The expression cassette is useful for producing peptide and

XX polypeptide in a cell, preferably a tandem polypeptide that forms an

XX inclusion body when expressed in a cell. The present sequence is that of

XX a DNA sequence which encodes a polypeptide which may be produced using

XX the expression cassette of the invention.

XX Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX expression cassette; tandem polypeptide; inclusion body;

XX inclusion body; fusion partner; PTH; gene; ds.

XX Unidentified.

XX WO2003100022-A2.

XX 04-DEC-2003.

XX 23-MAY-2003; 2003WO-US016645.

XX 24-MAY-2002; 2002US-0383212P.

XX (REST-) RESTORAGEN INC.

XX Xia Y, Peng L;

XX WPI; 2004-035129/03.

XX P-PSDB; ADJ65838.

XX New expression cassette comprising an operably linked nucleic acid

XX sequence, useful for producing a tandem polypeptide that forms an

XX inclusion body when expressed in a cell.

XX Disclosure; SEQ ID NO 34; 132pp; English.

XX The invention comprises an expression cassette which produces a tandem

XX polypeptide that form an inclusion body when expressed in a cell. The

XX expression cassette of the invention is useful for producing a peptide or

XX polypeptide in a cell, preferably a tandem polypeptide that forms an

XX inclusion body when expressed in a cell. The present DNA sequence encodes

XX a peptide which may be used in the construction of a tandem polypeptide

XX of the invention.

XX Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;

XX

XX

XX

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XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX expression cassette; tandem polypeptide; inclusion body;

XX inclusion body; fusion partner; PTH; gene; ds.

XX Unidentified.

XX WO2003100022-A2.

XX 04-DEC-2003.

XX 23-MAY-2003; 2003WO-US016645.

XX 24-MAY-2002; 2002US-0383212P.

XX (REST-) RESTORAGEN INC.

XX Xia Y, Peng L;

XX WPI; 2004-035129/03.

XX P-PSDB; ADJ65838.

XX New expression cassette comprising an operably linked nucleic acid

XX sequence, useful for producing a tandem polypeptide that forms an

XX inclusion body when expressed in a cell.

XX Disclosure; SEQ ID NO 34; 132pp; English.

XX The invention comprises an expression cassette which produces a tandem

XX polypeptide that form an inclusion body when expressed in a cell. The

XX expression cassette of the invention is useful for producing a peptide or

XX polypeptide in a cell, preferably a tandem polypeptide that forms an

XX inclusion body when expressed in a cell. The present DNA sequence encodes

XX a peptide which may be used in the construction of a tandem polypeptide

XX of the invention.

XX Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;

XX

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XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

PI Chen C, Xiu C, Li M;  
 XX WPI; 2004-09606/11.  
 DR P-PSDB; ADW14376.  
 XX  
 PT Production of reorganized human parathyroid hormone 1-34 peptide.  
 XX  
 PS Claim 3; SEQ ID NO 1; 25bp; Chinese.  
 CC The invention relates to a novel process for preparing recombinant human  
 CC parathyroxin 1-34 peptide, including such steps as culturing a host cell  
 CC in proper conditions, separating Gly-Ser-Pro-PTH 1-34 peptide (ADW14376),  
 CC severing by Pro endopeptidase to form PTH 1-34 peptide (ADW14378) and  
 CC separating and purifying PTH 1-34 peptide. The present sequence encodes  
 CC the Gly-Ser-Pro-PTH 1-34 peptide.  
 XX  
 SQ Sequence 111 BP; 31 A; 28 C; 25 G; 27 T; 0 U; 0 Other;  
 Query Match 64.5%; Score 60; DB 13; Length 111;  
 Best Local Similarity 57.6%; Pred. No. 1.6e-09;  
 Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;  
 QY 2 CUGUUUCCGAAAUCCAGCUGAUGCAGUGUGUGUGUGUGUCCAUAGAACUG 61  
 Db 11 CTGTTCTGTAATCCAGCTGATGCACAACCTGGGTAAACCTGAACTATGAGAACTG 70  
 QY 62 UUGAAGUGGUGGUGUAAAAAACUGCAGAGAGGU 93  
 Db 71 TTGAATGGCTGCGTAAAAAACTGCAGAGAGCTT 102

RESULT 11  
 ADG93260  
 ID ADG93260 standard; DNA; 117 BP.  
 XX  
 AC ADG93260;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Novel expression cassette-related PTH DNA SeqID141.  
 XX  
 KM expression cassette; high yield polypeptide production;  
 KM tandem polypeptide; inclusion body; gene; ds; PTH.  
 OS  
 OS Unidentified.  
 OS Synthetic.  
 OS  
 PN WO2003100021-A2.  
 XX  
 PD 04-DEC-2003.  
 XX  
 PF 23-MAY-2003; 2003WO-US016643.  
 XX  
 PR 24-MAY-2002; 2002US-0383370P.  
 XX  
 PA (BEST-) RESTORAGEN INC.  
 PA (HARL/) HARLEY S.  
 XX  
 PI Harley S, Williams JA, Luan P, Xia Y;  
 XX  
 DR WPI; 2004-035128/03.  
 DR P-PSDB; ADG93259.  
 XX  
 PT New expression cassette comprising an operably linked nucleic acid  
 PT sequence, useful for producing a tandem polypeptide that forms an  
 PT inclusion body when expressed in a cell.  
 XX  
 PS Disclosure; SEQ ID NO 141; 157bp; English.  
 XX  
 CC This invention relates to a novel expression cassette and methods for  
 CC high yield production of polypeptides. The cassette comprises an operably  
 CC linked nucleic acid sequence, where the expression of the cassette  
 CC produces a tandem polypeptide that forms an inclusion body when expressed

CC in a cell. The expression cassette is useful for producing peptide and  
 CC polypeptide in a cell, preferably a tandem polypeptide that forms an  
 CC inclusion body when expressed in a cell. The present sequence is that of  
 CC a DNA sequence which encodes a PTH peptide which was used in the  
 CC exemplification of the invention.  
 XX  
 SQ Sequence 117 BP; 35 A; 27 C; 25 G; 30 T; 0 U; 0 Other;  
 Query Match 64.5%; Score 60; DB 12; Length 117;  
 Best Local Similarity 57.6%; Pred. No. 1.7e-09;  
 Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;  
 QY 2 CUGUUUCCGAAAUCCAGCUGAUGCAGUGUGUGUGUGUCCAUAGAACUG 61  
 Db 2 CTGTTCTGTAATCCAGCTGATGCACAACCTGGGTAAACCTGAACTATGAGAACTG 61  
 QY 62 UUGAAGUGGUGGUGUAAAAAACUGCAGAGAGGU 93  
 Db 62 TTGAATGGCTGCGTAAAAAACTGCAGAGAGCTT 93

RESULT 12  
 AAT34865  
 ID AAT34865 standard; cDNA; 168 BP.  
 XX  
 AC AAT34865;  
 XX  
 DT 02-DEC-1996 (first entry)  
 XX  
 DE Plasmid pBN1:PTH(1-34)-C-1c portion encoding PTH(1-34) Cys.  
 XX  
 KM PTH; parathyroid hormone; parathormone; C-amide; C-amidated peptide;  
 KM alpha-carboxamide; recombinant protein; fusion protein; transpeptidation;  
 KM vector; plasmid pBN1; carbonic anhydrase II; ss.  
 XX  
 OS Synthetic.  
 OS  
 FH Key Location/Qualifiers  
 FT 1..162  
 FT CDS /\*tag= a  
 FT /product= "hCA-linker-PTH(1-34) Cys fusion"  
 XX  
 PN WO9617941-A2.  
 XX  
 PD 13-JUN-1996.  
 XX  
 PF 07-DEC-1995; 95WO-US015799.  
 XX  
 PR 07-DEC-1994; 94US-00350528.  
 XX  
 PA (BION-) BIONEERASKA INC.  
 PA  
 PI Stout JS, Patriidge BE, Heriksen DB, Holmquist B, Wagner FW;  
 XX  
 DR WPI; 1996-287185/29.  
 DR P-PSDB; AAR98967.  
 XX  
 PT Production of C-terminal alpha-carboxamidated peptide(s) - by cleavage  
 PT and transpeptidation of recombinant multicopy peptide(s) or fusion  
 PT constructs.  
 XX  
 PS Example 7; Fig 1; 93bp; English.  
 XX  
 CC A portion (AAT34865) of plasmid pBN1:PTH(1-34)-C-1c comprises DNA coding  
 CC for a fusion protein (AAR98967) composed of the C-terminal end of human  
 CC carbonic anhydrase II joined by an intrconnecting peptide (including a  
 CC thrombin cleavage site) to amino acids 1-34 of PTH (AAR98966), followed  
 CC by a Cys residue and C-terminal sequence. The complete construct can be  
 CC expressed in E. coli transformants. The intrconnecting peptide and C-  
 CC terminal Cys residue enable the recombinant protein construct to be  
 CC selectively reacted to produce C-terminal carboxamidated PTH(1-34)  
 CC  
 SQ Sequence 168 BP; 41 A; 44 C; 42 G; 41 T; 0 U; 0 Other;



[illegible]

Dn		62	TTGAATGGCTGCGTAAATAAAGCTGACGACGCT	93
<hr/>				
RESULT 14				
ID	ADJ65859		standard; DNA; 252 BP.	
XX	ADJ65859;			
XX				
DT	06-MAY-2004	(first entry)		
XX				
DE	PTH protein coding sequence.			
XX				
KW	expression cassette; tandem polypeptide; inclusion body;			
XX	inclusion body fusion partner; PTH; gene; ds.			
OS	Unidentified.			
XX				
PN	WO2003100022-A2.			
XX				
PD	04-DEC-2003.			
XX				
PF	23-MAY-2003; 2003WO-US016645.			
XX				
PR	24-MAY-2002; 2002US-0383212P.			
XX				
PA	(REST-) RESTORAGEN INC.			
Pt	Xia Y, Peng L;			
XX				
DR	WPI; 2004-035129/03.			
DR	P-PSDB; ADJ65839.			
XX				
PT	New expression cassette comprising an operably linked nucleic acid			
PT	sequence, useful for producing a tandem polypeptide that forms an			
PT	inclusion body when expressed in a cell.			
XX				
XX	Disclosure; SEQ ID NO 35; 132pp; English.			
CC				
CC	The invention comprises an expression cassette which produces a tandem			
CC	polypeptide that form an inclusion body when expressed in a cell. The			
CC	expression cassette of the invention is useful for producing a peptide or			
CC	polypeptide in a cell, preferably a tandem polypeptide that forms an			
CC	inclusion body when expressed in a cell. The present DNA sequence encodes			
CC	a protein which may be used in the construction of a tandem polypeptide			
CC	of the invention.			
XX				
SQ	Sequence 252 BP; 68 A; 65 C; 61 G; 58 T; 0 U; 0 Other;			
<hr/>				
Query Match	64.5%; Score 60; DB 12; Length 252;			
Best Local Similarity	57.6%; Pred. No. 2e-09;			
Matches	53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;			
Oy				
Db	2 CUGUUUCCGAUAUCCAGCUGAUGCACGUGUGUGUGUGUGUTCCAUGAACCG 61			
	:::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::			
	2 CTGTTTCGAATCCAGCTGATGCACAACCTGGGTAAACACTGAACCTCTATGAACTG 61			
Oy	62 UUGAUUGGUCUGUAUAAAAAUAUGAGAGACGU 93			
	::: :::   :::   :::   :::   :::   :::   :::   :::   :::   :::			
Db	62 TTGAATGGCTGCGTAAATAAAGCTGACGACGCT 93			
<hr/>				
RESULT 15				
ID	ADJ65913			
XX	ADJ65913 standard; DNA; 264 BP.			
XX	ADJ65913;			
XX				
DT	06-MAY-2004	(first entry)		
XX				
DE	Tandem polypeptide-encoding expression cassette #5.			
XX				
XX	expression cassette; tandem polypeptide; inclusion body;			

**KW** inclusion body fusion partner; gene; ds.

OS Unidentified.

PN WO2003100022-A2.

PD 04-DEC-2003.

PF 23-MAY-2003; 2003WO-US016645.

PR 24-MAY-2002; 2002US-0383212P.

PA (REST-) RESTORAGEN INC.

Xia Y, Peng L;

AA  
DR  
WPT: 2004-035129/03.

DR E-PSDB; ADJ065912.  
XX

PT sequence useful for producing a tandem polypeptide that forms an

inclusion body when expressed in a cell.

PS Disclosure; SEQ ID NO 89; 132pp; English.  
XX

cc The invention comprises an expression cassette

expression cassette of the invention is useful for producing a peptide polypeptide in a cell preferably a tandem polypeptide that forms an

CC inclusion body when expressed in a cell. The present DNA sequence

CC the invention.  
xy

Sequence 264 BP; 72 A; 67 C; 64 G; 61 T; 0 U; 0 Other;

```
Query Match 64.5%; Score 60; DB 12; Length 264;
```

Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY 2 CUGUUCCGAUCCAGCUGAUGCACGGUGGUGGUGGUGGUC

Db 5 CTGTTTCTGAATCCAGCTGATGCACCACTGGTTAAACACCTGAACCTTATGGAACGTG 64

QY 62 UUGAUGGCUCCGUAAAAACUGCAGGACGU 93

Db 65 TTGAATGGCTGCCGTAATAAACTGCAGGACGTT 96

Job time : 242.667 secs

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:35:17 ; Search time 1177.67 Seconds  
(without alignments)  
4488.911 Million cell updates/sec

Title: US-09-475-158A-15

Perfect score: 93  
Sequence: 1 gcguuuccgaacaacgacgu.....guaaaaacugcagacgu 93Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pt:\*  
9: gb\_to:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vt:\*  
14: gb\_ncg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	93	6	BD266833 PTH funct
2	83.4	89.7	93	6	BD266832 PTH funct
3	64.2	69.0	93	6	BD266834 PTH funct
4	56.8	61.1	258	6	AR269042 Sequence
5	54.2	58.3	141	6	AR005132 Sequence
6	54.2	58.3	141	6	AR005133 Sequence
7	54.2	58.3	141	6	AR177779 Sequence
8	54.2	58.3	141	6	AR177780 Sequence
9	54.2	58.3	207	6	AR043797 Sequence
10	51	54.8	717	6	A36847 Sequence 1
11	51	54.8	945	6	A36849 Sequence 1
12	50.4	54.2	405	6	BD234383 Recombina
13	50.4	54.2	408	6	BD234385 Recombina
14	50.4	54.2	408	6	BD234386 Recombina
15	50.4	54.2	411	6	BD234384 Recombina
16	50.4	54.2	414	6	BD234390 Recombina
17	50.4	54.2	417	6	BD234387 Recombina
18	50.4	54.2	423	6	BD234388 Recombina

19	50.4	54.2	435	6	BD234389	BD234389 Recombina
20	46.2	49.7	252	6	AR027046	AR027046 Sequence
21	46.2	49.7	252	6	E05675	E05675 DNA encodin
22	44.6	48.0	252	6	AR027011	AR027011 Sequence
23	44.6	48.0	252	6	AR027044	AR027044 Sequence
24	44.6	48.0	252	6	AR030635	AR030635 Sequence
25	44.6	48.0	252	6	AR168173	AR168173 Sequence
26	44.6	48.0	252	6	E05658	E05658 DNA encodin
27	44.6	48.0	252	6	E05673	E05673 DNA encodin
28	44.6	48.0	252	6	I83594	I83594 Sequence 1
29	44.6	48.0	253	6	AR027020	AR027020 Sequence
30	44.6	48.0	253	6	E04335	E04335 Synthetic D
31	44.6	48.0	253	6	E05671	E05671 DNA encodin
32	44.6	48.0	253	6	I83595	I83595 Sequence 3
33	44.6	48.0	253	11	S71759	S71759 human parat
34	44.6	48.0	255	6	AR027021	AR027021 Sequence
35	44.6	48.0	255	6	E05672	E05672 DNA encodin
36	44.6	48.0	255	6	I83596	I83596 Sequence 4
37	43.4	46.7	74	6	AR043802	AR043802 Sequence
38	43	46.2	67	6	A79761	A79761 Sequence 9
39	43	46.2	67	6	AR135774	AR135774 Sequence
40	43	46.2	102	6	BD170195	BD170195 Process f
41	43	46.2	186	6	BD170222	BD170222 Process f
42	43	46.2	201	6	BD170213	BD170213 Process f
43	43	46.2	225	6	BD170211	BD170211 Process f
44	43	46.2	240	6	BD170198	BD170198 Process f
45	43	46.2	252	6	AR027050	AR027050 Sequence

## ALIGNMENTS

RESULT 1  
BD266833 93 bp RNA linear PAT 17-JUN-2003  
LOCUS PTH functional domain conjugate peptides, derivatives thereof and  
DEFINITION novel tethered ligand-receptor molecules.  
ACCESSION BD266833.1 GI:33076601  
VERSION JP 2002533115-A/2.  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 93)  
AUTHORS Gardella,T.T., Kronenberg,H.M., Potts,J.T. and Jueppner,H.  
TITLE PTH functional domain conjugate peptides, derivatives thereof and  
JOURNAL novel tethered ligand-receptor molecules  
Patent: JP 2002533115-A 2 08-OCT-2002;  
THE GENERAL HOSPITAL CORP  
COMMENT OS Artificial Sequence  
PN JP 2002533115-A/2  
PD 08-OCT-2002  
PF 31-DEC-1999 JP 2000591171  
PR 31-DEC-1998 US 60/114577  
PI THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD PI  
JUEPPNER  
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P5/18,A61P19/08, PC  
PC C12N15/10,A61P19/10,  
PC A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC  
C12N1/21,  
PC C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC  
Description of Artificial Sequence: modified PTH sequence FH Key  
Location/Qualifiers  
FT 1..93  
FT 7 source /organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..93  
/organism='synthetic construct'  
/mol\_type='genomic RNA'  
/db\_xref='taxon:32630'  
ORIGIN  
Query Match 100.0%; Score 93; DB 6; Length 93;



Db 2 CTGTTTGGAAATCCAGCTTATGATGATACTGGGTAAACATCTGAACTCGATGAGACGTG 61  
Qy 62 UUGAUGGCGUCGUAAAAAUCUGCAGACGU 93  
Db 62 TTGAATGGCTGCGTAAAAAACTGCAGAGATGTT 93

RESULT 5  
AR005132  
LOCUS AR005132 141 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 3 from patent US 5747453.  
ACCESSION AR005132  
VERSION AR005132.1 GI:3966011  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
FEATURES  
REFERENCE 1 (bases 1 to 141)  
AUTHORS Holladay,L.A. and Oldenburg,K.R.  
TITLE Method for increasing the electrotransport flux of polypeptides  
JOURNAL Patent: US 5747453-A 3 05-MAY-1998;  
LOCATION/Qualifiers  
1. .141  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 58.3%; Score 54.2; DB 6; Length 141;  
Best Local Similarity 56.0%; Pred. No. 1.9e-05;  
Matches 51; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

Qy 2 CUGUUCGGAUAUCCAGCUGAUGCAGGUGUGUGUGUGUGUCCAUUGAAGCG 61  
Db 26 CCGTTCCGAATCCAGCTGCTGCACAACTGGGTAAACACTGAATCCTCGAGCGTG 85

Qy 62 UUGAUGGCGUCGUAAAAAUCUGCAGACGU 92  
Db 86 TTGAATGGCTGCGTAAAAAACTGCAGAGCGT 116

RESULT 6  
AR005133  
LOCUS AR005133 141 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 5 from patent US 5747453.  
ACCESSION AR005133  
VERSION AR005133.1 GI:3966012  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
FEATURES  
REFERENCE 1 (bases 1 to 141)  
AUTHORS Holladay,L.A. and Oldenburg,K.R.  
TITLE Method for increasing the electrotransport flux of polypeptides  
JOURNAL Patent: US 5747453-A 5 05-MAY-1998;  
LOCATION/Qualifiers  
1. .141  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 58.3%; Score 54.2; DB 6; Length 141;  
Best Local Similarity 56.0%; Pred. No. 1.9e-05;  
Matches 51; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

Qy 2 CUGUUCGGAUAUCCAGCUGAUGCAGGUGUGUGUGUGUCCAUUGAAGCG 61  
Db 116 CCGTTCCGAATCCAGCTGCTGCACAACTGGGTAAACACTGAATCCTCGAGCGTG 57

Qy 62 UUGAUGGCGUCGUAAAAAUCUGCAGACGU 92  
Db 56 TTGAATGGCTGCGTAAAAAACTGCAGAGCGT 26

RESULT 7  
AR177779  
LOCUS AR177779 141 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 3 from patent US 6313092.  
ACCESSION AR177779  
VERSION AR177779.1 GI:17920134  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
FEATURES  
REFERENCE 1 (bases 1 to 141)  
AUTHORS Holladay,L.A. and Oldenburg,K.R.  
TITLE Method for increasing the electrotransport flux of polypeptides  
JOURNAL Patent: US 6313092-A 3 06-NOV-2001;  
LOCATION/Qualifiers  
1. .141  
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/mol\_type="unassigned DNA"

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Best Local Similarity 56.0%; Pred. No. 1.9e-05;  
Matches 51; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

Qy 2 CUGUUCGGAUAUCCAGCUGAUGCAGGUGUGUGUGUGUCCAUUGAAGCG 61  
Db 26 CCGTTCCGAATCCAGCTGCTGCACAACTGGGTAAACACTGAATCCTCGAGCGTG 85

Qy 62 UUGAUGGCGUCGUAAAAAUCUGCAGACGU 92  
Db 86 TTGAATGGCTGCGTAAAAAACTGCAGAGCGT 116

RESULT 8  
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LOCUS AR177780 141 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 5 from patent US 6313092.  
ACCESSION AR177780  
VERSION AR177780.1 GI:17920135  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
FEATURES  
REFERENCE 1 (bases 1 to 141)  
AUTHORS Holladay,L.A. and Oldenburg,K.R.  
TITLE Method for increasing the electrotransport flux of polypeptides  
JOURNAL Patent: US 6313092-A 5 06-NOV-2001;  
LOCATION/Qualifiers  
1. .141  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 58.3%; Score 54.2; DB 6; Length 141;  
Best Local Similarity 56.0%; Pred. No. 1.9e-05;  
Matches 51; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

Qy 2 CUGUUCGGAUAUCCAGCUGAUGCAGGUGUGUGUGUGUCCAUUGAAGCG 61  
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Qy 62 UUGAUGGCGUCGUAAAAAUCUGCAGACGU 92  
Db 56 TTGAATGGCTGCGTAAAAAACTGCAGAGCGT 26

RESULT 9  
AR043797  
LOCUS AR043797 207 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 8 from patent US 5814603.  
ACCESSION AR043797  
VERSION AR043797.1 GI:5964805  
KEYWORDS

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LOCUS	BD234386	408 bp	DNA	linear PAT 17-JUL-2003
DEFINITION	Recombinant synthesis of beta-lipotropin and other peptides.			
ACCESSION	BD234386.1	GI:33044156		
VERSION	JP 2002533072-A/7.			
KEYWORDS	UP 2002533072-A/7.			
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
REFERENCE	other sequences; artificial sequences.			
AUTHORS	1 (bases 1 to 408)			
TITLE	Hale,J.E., Hersherberger,C.L., Larson,J.L. and Menke,M.A.			
JOURNAL	Recombinant synthesis of beta-lipotropin and other peptides Patent: JP 2002533072-A 7 Oct-2002; Eli Lilly AND CO			
COMMENT	OS Artificial Sequence			
	PN JP 2002533072-A/7			
	PD 08-OCT-2002			
	PF 15-DEC-1999 JP 2000589671			
	PR 21-DEC-1998 US 60/113058			
	PI JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON,			
	PI MICHAEL ANDREW MENKE			
	PC C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC			
	,C12N6/10,C12N9/50,			
	PC C12P21/02,C12N15/00,C12M5/00			
	CC Description of Artificial Sequence: PCB-LVFR-hPTH fusion FH			
	Key Location/Qualifiers			
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Query Match	54.2%; Score 50.4; DB 6;	Length 408;		
Best Local Similarity	52.2%; Pred. No. 0.00025;			
Matches 48; Conservative 18; Mismatches 26; Indels 0; Gaps 0;				
Oy	2 CUGUUCGGAUAUCCAGCUGAUGCACGGUGUGUGUGUGUCCAUUGAACGUG 61			
Db	296 CTGTTCCTGAATCAACTGATGCATAACCTGGCGCAAACTGAACCTTATGAGCGTG 355			
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Db	356 TAGAATGCGCTGCCGTAAAGAAGCTGCAGATGTT 387			
RESULT 15				
LOCUS	BD234384	411 bp	DNA	linear PAT 17-JUL-2003
DEFINITION	Recombinant synthesis of beta-lipotropin and other peptides.			
ACCESSION	BD234384			
VERSION	BD234384.1	GI:33044154		





GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:36:53 ; Search time 1823 Seconds  
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2386.834 Million cell updates/sec

Title: US-09-475-158A-15

Perfect score: 1 gcuuuuccgaauccagcu.....guaaaaacugcagcagcu 93

Scoring table: IDENTITY NUC  
Gap0 10\_0, Gapex1 1\_0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_est4.\*  
5: gb\_est5.\*  
6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_est9.\*  
10: gb\_est10.\*  
11: gb\_est11.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	38.8	41.7	316	1	AA372113
3	38.8	41.7	324	8	W19763
4	38.2	41.1	352	8	W39062
5	38.2	41.1	376	8	W38966
6	38.2	41.1	411	8	W37708
7	38.2	41.1	416	8	W31998
8	38.2	41.1	434	8	W38764
9	38.2	41.1	450	8	W56235
10	38.2	41.1	453	8	W33077
11	38.2	41.1	466	8	W56820
12	38.2	41.1	536	8	W19765
13	38.2	41.1	576	8	W56120
14	38.2	41.1	583	9	W39202
15	38.2	41.1	702	9	BH958789
16	38.2	41.1	721	2	BG198564
17	38.2	41.1	741	1	AI051997
18	38.2	41.1	757	5	BX106232
19	38.2	41.1	809	2	BG188276
20	38.2	41.1	820	5	BX103059
21	37.2	40.0	780	1	AI028087
22	36.6	39.4	523	8	W52945

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C	27	36.6	39.4	323	3	BE482262	BE482262	167989	BA
C	28	36.6	39.4	393	1	AM658405	AM658405	94407	MAR
C	29	36.6	39.4	397	1	AM484007	AM484007	58088	MAR
C	30	36.6	39.4	398	8	DN347669	DN347669	LIB3578-0	
C	31	36.6	39.4	411	3	BI542423	BI542423	456931	MA
C	32	36.6	39.4	413	8	DN348158	DN348158	LIB3578-0	
C	33	36.6	39.4	431	8	DN349208	DN349208	LIB3578-0	
C	34	36.6	39.4	435	2	BF230607	BF230607	252377	BA
C	35	36.6	39.4	439	8	DN347054	DN347054	LIB3578-0	
C	36	36.6	39.4	442	8	DN346969	DN346969	LIB3578-0	
C	37	36.6	39.4	447	8	DN347081	DN347081	LIB3578-0	
C	38	36.6	39.4	451	8	DN346863	DN346863	LIB3578-0	
C	39	36.6	39.4	451	8	DN347334	DN347334	LIB3578-0	
C	40	36.6	39.4	458	8	DN347142	DN347142	LIB3578-0	
C	41	36.6	39.4	459	8	DN347234	DN347234	LIB3578-0	
C	42	36.6	39.4	460	1	AV593657	AV593657	AV593657	
C	43	36.6	39.4	461	2	BG691533	BG691533	340736	BA
C	44	36.6	39.4	462	8	DN347146	DN347146	LIB3578-0	
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#### ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION  
EST83988 Human Parathyroid gland Homo sapiens cDNA 5' end similar to parathyroid hormone (HT:2194), mRNA sequence.  
T29548  
T29548.1 GI:611646

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE

AUTHORS

TITLE  
JOURNAL  
PUBMED  
COMMENT

Other ESTs: THC23168  
Contact: Venter, JC  
The Institute for Genomic Research  
932 Clopper Rd, Gaithersburg, MD 20878  
Tel: 3016699056  
Fax: 3016699423  
Email: tcdinfo@tigr.org  
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tcdinfo@tigr.org)

Page 2

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/db_xref="ATCC (inhost):106648"
/db_xref="taxon:9606"
/clone_lib="Human Parathyroid gland"
/note="Organ: parathyroid gland"

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Best Local Similarity 48.4%; Pred. No. 0.12;  
Matches 44; Conservative 14; Mismatches 33; Indels 0; Gaps 0;

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2 CTGCTTUUCCGAAGAACCGACGUGUGUGUGUGUGUGUGUGUGUCCAAGAACG 61

Dd  
166 CTGTGAGTGTAATACAGCTTATGCATTAACTNGAAAAACATCTNANCTCGAATGGAGAGAG 225

Oy      62 TUGAATGGCGUCGUAATAAACTUCAGGACGT    92  
         : |||:||||:|||||:  
Db      226 TAGAATGGCTGCCTAAGAAGCTGCAGGATGT    256

RESULT 2	LOCUS	DEFINITION
AA372113	316 bp	parathyroid gland tumor II Homo sapiens cDNA 5' end similar to parathyroid hormone, mRNA sequence.

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ACCEPTED FOR PUBLICATION  AA372113.1  GI:2024432
VERSION

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KEYWORDS	DOI
SOURCE	Homo sapiens (human)

**SOURCE**  
**ORGANISM**

Euryzoa; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 316)

## REFERENCE AUTHORS

nominales; nomio:  
1 (bases 1 to 316)  
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bale, C.O., Lee, N.A., Alkness, B.F., Weisbrock, A.S., Gage, D.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Georgiagen, N.S., Gloder, A., Gnehm, C.L., Hanna, M.C., Heddlom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Namaros, S.T., Merrick, J.M., Moreno-Palmarum, R.F., McDonald, L.A., Nauven, D.T., Perichino, S.M.

**TITLE** Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
**JOURNAL** *Nature* 377 (6547 Suppl), 3-174 (1995)  
**FLASKS, C.M., and VENTER, J.C.**

**PUBLISHED  
COMMENT**

contact: [neirav@bioinformatics.org](mailto:neirav@bioinformatics.org), <http://www.bioinformatics.org>

The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056  
Fax: 3018699423

Email: [arkerlav@tigr.org](mailto:arkerlav@tigr.org)  
For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse.  
Location/Qualifiers

**Source**

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Site_1: EcoRI; Site_2: XhoI"

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Matches 44;	Conservative 14;	Mismatches 33;	Indels 0;	Gaps 0;

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Oy      62  TUGAUGCGUCGCGUAAAAAACUGCAGCAGCGU  92
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	Zb39601.r1	Soares parathyroid tumor NHPPA Homo sapiens	cDNA clone
	IMAGE:3055952.5	similar to gp:v00597 PARATHYROID HORMONE PRECURSOR	

ACCESSION W19763

KEYWORDS

ORGANISM	Homo sapiens
BOOKED	Homo sapiens (human)

Eumetazoa, Metazoa, Cnidaria, Vertebrata, Echinodermata, Mollusca, Eutheria; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

## REFERENCE

ACHONKS  
HILLIER, D., CLARK, N., DUBUQUE, I., ELLISTON, K., HAWKINS, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Faloutsos, D., Kilkun, D., Kollman, J., Soares, W., Tan, E.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and

TITLE The WashU-Merck EST Project

JOURNAL  
COMMENT

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1890  
Fax: 314 286 1890  
Email: [estewatson@wustl.edu](mailto:estewatson@wustl.edu)  
This clone is available royalty-free through INLH; contact the  
IMAG Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: [mob.RC6A+ET](#)  
High quality sequence [stop: 222](#).

**REMARKS**  
**SOURCE**

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1. .324

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/cd /x1el=...caxon:2006...
/clone="IMAGE:305952"
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/dev stage="adult"
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/clone lib="Soares parathyroid tumor NbHPA"
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(pharmacica) with a modified polylinker: site 1: Not I;
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site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer

TTTTT-3']. double-stranded cDNA was size selected, ligated









Scores and M. Fatima Bernaldo: RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

Query Match	41.1%;	Score 38.2;	DB 8;	Length 536;
Best Local Similarity	48.4%;	Pred. No. 0.47;	Mismatches	44;
Conservative	14;	Indels	0;	Gaps 0.

2 CUGGDUUCCGAUAUCCAGCUGAUCCAGCUGUGUGUGUGUGUGUCCAUCAUGAACUG 61

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QY 62 UUGAUGCGUCGUAAAAACUGCAGACGCU 92  
: |||: |||: ||| : ||| ||| :  
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LOCUS	576 bp	RNA	linear	EST 11-OCT-1996
DEFINITION	z656b6.r1 Soares parathyroid tumor NbhPA Homo sapiens cDNA clone			
IMAGE:326363	5' similar to gp:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.			
ACCESSION	W56120			
VERSION	W56120.1	GI:1358009		

ACCESSION	W56120
VERSION	W56120.1
KEYWORDS	GI:1358009
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Fukarya: Metazoa:

REFERENCE  
AUTHORS  
1 (bases 1 to 576)  
Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holtman, M., Hultman, M., Kucab, T., Le, M., Lennon, G., Matra, M.,  
Persons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and  
Wilson, R.  
TITLE  
The Washu-Merck EST Project  
AUTHOR  
Submitted (1995)

TITLE The Mashu-Merck EST Project  
 JOURNAL Unpublished (1995)  
 CONTACT: Wilson RK  
 COMMENT Washington University School of Medicine  
 444 East Park Parkway, Box 8501, St. Louis, MO 63108

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [estewatson.wustl.edu](mailto:estewatson.wustl.edu)  
This clone is available royally-free through LNL; contact the  
IMAG Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.  
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Seq primer: mob.REGA+ET  
High quality sequence drop: 433.

## Loc: 1

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Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer
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TTTT-3', double-stranded cDNA was size selected, ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pRTT3
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. library constructed by Bento

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Search completed: November 24, 2005, 01:30:29  
Job time : 1824 secs

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**This Page Blank (uspto)**



Fri Nov 25 10:36:37 2005

us-09-475-158a-15.rni

Page 2

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,275
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,651
REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
TELEFAX: (415) 496-8048
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 7..138
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 25

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[illegible]

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/468,275
3 FILING DATE: 06-JUN-1995
4 CLASSIFICATION: 514
5 ATTORNEY/AGENT INFORMATION:
6 NAME: MILLER, D. BYRON
7 REGISTRATION NUMBER: 30,661
8 REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: (415) 496-8150
11 TELEFAX: (415) 496-8048
12 INFORMATION FOR SEQ ID NO: 5:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 141 base pairs
15 TYPE: nucleic acid
16 STRANDEDNESS: single
17 TOPOLOGY: linear
18 MOLECULE TYPE: DNA (genomic)
19 US-08-468-275-5

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Db              56 TTGAATGCTGCTATAAAAAC TGACGAGGACGT 26

RESULT 4
US-09-007-466-3
Sequence 3, Application US/09007466
Patent No. 6313092
GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,466
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,275
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
TELEFAX: (415) 496-8048
INFORMATION FOR SEQ ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
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/ Patent No. 6333189
/ GENERAL INFORMATION:
/ APPLICANT: HOLLADAY, LESLIE A.
/ APPLICANT: OLDENBURG, KEVIN R.
/ TITLE OF INVENTION: METHOD FOR INCREASING THE
/ TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ALZA CORPORATION
/ STREET: 950 PAGE MILL ROAD
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94303-0802
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/952,980B
/ FILING DATE: 20-NOV-1997
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MILLER, D. BYRON
/ REGISTRATION NUMBER: 30,661
/ REFERENCE/DOCKET NUMBER: 2349 CIP 1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 496-8150
/ TELEFAX: (650) 496-8048
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 141 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-952-980B-5

Query Match          58.3%; Score 54.2; DB 3; Length 141;
Best Local Similarity 56.0%; Pred. No. 1.9e-08;
Matches 51; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

QY      2 CUGUUNCCGAUAUCCAGCUGAUGGUGUGUGUGUGUGUGUCCAUUGAAGCUG 61
Db      116 CCGTTCCGAATCCAGCTGCTGCAACAACCTGGGTAAACCTGAACCTCCCTCGAGCGTG 57
QY      62 UUGAUAUGGUGUGUAAAAAACUGCAGACG 92
Db      56 TTGAATGCTGCTGTAATAAACTGCAGACG 26

RESULT 8
US-08-142-551B-8
/ Sequence 8, Application US/08142551B
/ Patent No. 5814603
/ GENERAL INFORMATION:
/ APPLICANT: Oldenburg, Kevin R.
/ APPLICANT: Selick, Harold E.
/ TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
/ TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
/ NUMBER OF SEQUENCES: 132
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Burns, Doane, Swecker & Mathis
/ STREET: 699 Prince Street
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: US
/ ZIP: 22313
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
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/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/142,551B
/ FILING DATE: 25-OCT-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/077,296
/ FILING DATE: 14-JUN-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/898,219
/ FILING DATE: 12-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/965,677
/ FILING DATE: 22-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Swiss, Gerald F.
/ REGISTRATION NUMBER: 30,113
/ REFERENCE/DOCKET NUMBER: 000324-010
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 854-8275
/ TELEFAX: (415) 854-7400
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 207 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..201
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1..51
/ OTHER INFORMATION: /note= "Encodes the leader peptide
/ OTHER INFORMATION: sequence that serves to direct the protein into
/ OTHER INFORMATION: inclusion bodies."
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 70..174
/ OTHER INFORMATION: /note= "Encodes the protein or
/ OTHER INFORMATION: peptide of interest"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 175..207
/ OTHER INFORMATION: /note= "Encodes amino acid sequence
/ OTHER INFORMATION: having six histamines that serves as a tag for the
/ OTHER INFORMATION: purification of the protein on a nickel column."
/ US-08-142-551B-8

Query Match          58.3%; Score 54.2; DB 2; Length 207;
Best Local Similarity 56.0%; Pred. No. 2.2e-08;
Matches 51; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

QY      2 CUGUUNCCGAUAUCCAGCUGAUGGUGUGUGUGUGUCCAUUGAAGCUG 61
Db      71 CCGTTCCGAATCCAGCTGCTGCAACAACCTGGGTAAACCTGAACCTCCCTCGAGCGTG 130
QY      62 UUGAUAUGGUGUAAAAAACUGCAGACG 92
Db      131 TTGAATGCTGCTGTAATAAACTGCAGACG 161

RESULT 9
US-08-733-446-58
/ Sequence 58, Application US/08733446
/ Patent No. 5856138
/ GENERAL INFORMATION:
/ APPLICANT: FUKUDA, Tsunehiko
/ TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTAINS AND
/ TITLE OF INVENTION: PRODUCTION THEREOF
/ NUMBER OF SEQUENCES: 62
/ CORRESPONDENCE ADDRESS:
```

```

ADDRESS: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,446
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/402,970
FILING DATE:
APPLICATION NUMBER: US/07/926,787
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 42025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..252
NAME/KEY: mutation
LOCATION: 19..24
IDENTIFICATION METHOD: E
US-08-733-446-58

Query Match          49.7%; Score 46.2; DB 2; Length 252;
Best Local Similarity 50.5%; Pred. No. 9,7e-06;
Matches 46; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY      2 CUGUUUCCGAUAUCCAGCUGAUGCAGGUGUGUGUGUGUGUCCAUUGAAGCGUG 61
       1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      2 CTGTGTCGAGATTCAGTCTGCTGCTTAACCTTGCGAACAATTGAACTGCATGAGCGTG 61
       1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      62 UUGAUGGCGUGCGUAAAAACUGCGAGCGU 92
       1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      62 TAGAATGCTGCGTAAGAAAGTTGACGAGATGT 92
       1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-10-340-484-14
Sequence 14, Application US/10340484
Patent No. 6875739
GENERAL INFORMATION:
APPLICANT: Stewart, Andrew F.
TITLE OF INVENTION: Treatment of Bone Disorders with Skeletal Anabolic
TITLE OF INVENTION: Drugs
FILE REFERENCE: 25200-501
CURRENT APPLICATION NUMBER: US/10/340,484
CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 60/347,215
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: 60/353,296
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 60/368,955

```

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PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/379,125
PRIOR FILING DATE: 2002-05-08
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 102
TYPE: DNA
ORGANISM: Homo sapiens
US-10-340-484-14

Query Match          48.0%; Score 44.6; DB 3; Length 102;
Best Local Similarity 49.5%; Pred. No. 2,5e-05;
Matches 45; Conservative 17; Mismatches 29; Indels 0; Gaps 0;

QY      2 CUGUUUCCGAUAUCCAGCUGAUGCAGGUGUGUGUGUGUGUCCAUUGAAGCGUG 61
       1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      2 CTGTGTCGAGATTCAGTCTGCTGCTTAACCTTGCGAACAATTGAACTGCATGAGCGTG 61
       1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      62 UUGAUGGCGUGCGUAAAAACUGCGAGCGU 92
       1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      62 TAGAATGCTGCGTAAGAAAGTTGACGAGATGT 92
       1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-08-689-190-1
Sequence 1, Application US/08689190
Patent No. 5714349
GENERAL INFORMATION:
APPLICANT: FUKUDA, Tsunehiko
APPLICANT: OSHIKA, Yuri
APPLICANT: YAMADA, Takao
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR HUMAN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,190
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/006,197
FILING DATE:
APPLICATION NUMBER: US/08/016,171
FILING DATE:
APPLICATION NUMBER: US/07/765,371
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, Gregory D
REGISTRATION NUMBER: 30,901
REFERENCE/DOCKET NUMBER: 41,288
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthesizing DNA

```

```

FEATURE:
NAME/KEY: CDS
LOCATION: 1..252
IDENTIFICATION METHOD: E
FEATURE:
NAME/KEY: MUTATION
LOCATION: 7, 8, 9, 12, 15, 19, 21, 33, 36, 43, 51, 58, 60,
IDENTIFICATION METHOD: S
US-08-689-190-1

Query Match
Best Local Similarity 48.0%; Score 44.6; DB 2; Length 252;
Best Local Similarity 49.5%; Pred. No. 3.2e-05;
Matches 45; Conservative 17; Mismatches 29; Indels 0; Gaps 0;

QY 2 CUGUUCGGAUCCAGCUGAUGACGUGUGUGUGUGUGUGUCCAUAGAACGUG 61
Db 2 CUGUUCGGAUCCAGCUGAUGACGUGUGUGUGUGUGUGUCCAUAGAACGUG 61
QY 62 UUGAUGGCGUGGUAACUAGCAGAGCU 92
Db 62 TAGAATGCTGCTGAAGAGTTGACAGAGTGT 92

RESULT 12
US-08-733-446-23
Sequence 23; Application US/08733446
Patent No. 5856138
GENERAL INFORMATION:
APPLICANT: FUKUDA, Tsunehiko
TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTELINS AND
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,446
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/402,970
FILING DATE:
APPLICATION NUMBER: US/07/926,787
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 42025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRP UR
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..252
IDENTIFICATION METHOD: E

US-08-733-446-23
Sequence 56; Application US/08733446
Patent No. 5856138
GENERAL INFORMATION:
APPLICANT: FUKUDA, Tsunehiko
TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTELINS AND
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,446
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/402,970
FILING DATE:
APPLICATION NUMBER: US/07/926,787
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 42025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRP UR
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 103...105
IDENTIFICATION METHOD: E

Query Match
Best Local Similarity 48.0%; Score 44.6; DB 2; Length 252;
Best Local Similarity 49.5%; Pred. No. 3.2e-05;
Matches 45; Conservative 17; Mismatches 29; Indels 0; Gaps 0;
```





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Page 8

Query Match	49.0%	Score 44.6	DB 3	Length 252
Best Local Similarity	49.5%	Pred. No. 3,2e-05		
Matches	45	Conservative 17	Mismatches 29	Indels 0
			Gaps	0
Qy	2	CUUUUUCGAAUUCAGCUCGACGUGUGUGUGUGUGUUCAGAAACUG	61	
Db	2	CTGTGTCGAGATCTGTTAACTGCACTTGGCAAACTTTGAATCCATGAGCGTG	61	
Qy	62	UUGAUGCGUCGUGUAAAAACUGCAGCAGU	92	
Db	62	TAGAAATGCTGCTTAAAGATGGCAGAGATGT	92	

Search completed: November 24, 2005, 01:34:14  
Job time : 73.6667 secs

Job time : 73.6667 secs



```

/ APPLICANT: Wagner, F.
/ APPLICANT: Peng, L.
/ APPLICANT: Xia, U.
/ APPLICANT: Holmquist, B.
/ TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
/ FILE REFERENCE: 1627.009US1
/ CURRENT APPLICATION NUMBER: US/10/997,700
/ PRIOR FILING DATE: 2004-11-24
/ PRIOR APPLICATION NUMBER: US 60/383,212
/ NUMBER OF SEQ ID NOS: 93
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 33
/ LENGTH: 102
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: PTH(1-34).
US-10-997-700-33

Query Match
Best Local Similarity 57.6%; Score 60; DB 9; Length 102;
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
```

```

/ APPLICANT: Wagner, F.
/ APPLICANT: Peng, L.
/ APPLICANT: Xia, U.
/ APPLICANT: Holmquist, B.
/ TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
/ FILE REFERENCE: 1627.009US1
/ CURRENT APPLICATION NUMBER: US/10/997,700
/ PRIOR FILING DATE: 2004-11-24
/ PRIOR APPLICATION NUMBER: US 60/383,212
/ NUMBER OF SEQ ID NOS: 93
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 33
/ LENGTH: 102
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: PTH(1-34).
US-10-997-700-33

Query Match
Best Local Similarity 57.6%; Score 60; DB 9; Length 102;
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
```

```

/ APPLICANT: Wagner, F.
/ APPLICANT: Peng, L.
/ APPLICANT: Xia, U.
/ APPLICANT: Holmquist, B.
/ TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
/ FILE REFERENCE: 1627.010US1
/ CURRENT APPLICATION NUMBER: US/10/997,078
/ PRIOR FILING DATE: 2004-11-24
/ PRIOR APPLICATION NUMBER: PCT/US03/16643
/ PRIOR FILING DATE: 2003-05-23
/ PRIOR APPLICATION NUMBER: US 60/383,370
/ NUMBER OF SEQ ID NOS: 148
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 61
/ LENGTH: 111
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: PTH(1-37).
US-10-997-078-61

Query Match
Best Local Similarity 57.6%; Score 60; DB 9; Length 111;
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
```

```

/ APPLICANT: Wagner, F.
/ APPLICANT: Peng, L.
/ APPLICANT: Xia, U.
/ APPLICANT: Holmquist, B.
/ TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
/ FILE REFERENCE: 1627.009US1
/ CURRENT APPLICATION NUMBER: US/10/997,700
/ PRIOR FILING DATE: 2004-11-24
/ PRIOR APPLICATION NUMBER: US 60/383,212
/ NUMBER OF SEQ ID NOS: 93
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 33
/ LENGTH: 102
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: PTH(1-34).
US-10-997-700-33

Query Match
Best Local Similarity 57.6%; Score 60; DB 9; Length 102;
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
```

```

/ APPLICANT: Wagner, F.
/ APPLICANT: Peng, L.
/ APPLICANT: Xia, U.
/ APPLICANT: Holmquist, B.
/ TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
/ FILE REFERENCE: 1627.009US1
/ CURRENT APPLICATION NUMBER: US/10/997,700
/ PRIOR FILING DATE: 2004-11-24
/ PRIOR APPLICATION NUMBER: US 60/383,212
/ NUMBER OF SEQ ID NOS: 93
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 34
/ LENGTH: 111
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: PTH(1-37)).
US-10-997-700-34

Query Match
Best Local Similarity 57.6%; Score 60; DB 9; Length 111;
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
```

```

/ APPLICANT: Wagner, F.
/ APPLICANT: Peng, L.
/ APPLICANT: Xia, U.
/ APPLICANT: Holmquist, B.
/ TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
/ FILE REFERENCE: 1627.010US1
/ CURRENT APPLICATION NUMBER: US/10/997,078
/ PRIOR FILING DATE: 2004-11-24
/ PRIOR APPLICATION NUMBER: PCT/US03/16643
/ PRIOR FILING DATE: 2003-05-23
/ PRIOR APPLICATION NUMBER: US 60/383,370
/ NUMBER OF SEQ ID NOS: 148
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 141
/ LENGTH: 117
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: A synthetic PTH sequence.
US-10-997-078-141

Query Match
Best Local Similarity 57.6%; Score 60; DB 9; Length 117;
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
```

```

/ APPLICANT: Wagner, F.
/ APPLICANT: Peng, L.
/ APPLICANT: Xia, U.
/ APPLICANT: Holmquist, B.
/ TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
/ FILE REFERENCE: 1627.010US1
/ CURRENT APPLICATION NUMBER: US/10/997,078
/ PRIOR FILING DATE: 2004-11-24
/ PRIOR APPLICATION NUMBER: PCT/US03/16643
/ PRIOR FILING DATE: 2003-05-23
/ PRIOR APPLICATION NUMBER: US 60/383,370
/ NUMBER OF SEQ ID NOS: 148
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 141
/ LENGTH: 117
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: A synthetic PTH sequence.
US-10-997-078-141

Query Match
Best Local Similarity 57.6%; Score 60; DB 9; Length 117;
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
```



```
; ORGANISM: Artificial Sequence
;
; FEATURE:
;   OTHER INFORMATION: Nucleotide sequence of a chimeric synthetic protein
US-10-997-762-18
```

Query Match	64.5%;	Score 60;	DB 9;	Length 276;
Best Local Similarity	57.6%;	Pred. No. 8.2e-11;		
Matches 53;	Conservative 19;	Mismatches 20;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 10
US-10-997-822-3
? Sequence 3, Application US/10997822
? Publication No. US2005027314A1
? GENERAL INFORMATION:
? APPLICANT: Holmquist, B.
? APPLICANT: Strydom, D.
? APPLICANT: Genesalk, X.
? APPLICANT: Cyser, R.
? TITLE OF INVENTION: POLYPEPTIDE CLEAVAGE PROCESS
? FILE REFERENCE: 1627.01US1
? CURRENT APPLICATION NUMBER: US/10/997,822
? CURRENT FILING DATE: 2004-11-24
? PRIOR APPLICATION NUMBER: PCT/US03/16647
? PRIOR FILING DATE: 2003-05-23
? PRIOR APPLICATION NUMBER: US 60/383,484
? PRIOR FILING DATE: 2002-05-24
? NUMBER OF SEQ ID NOS: 9
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO. 3
? LENGTH: 276
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Nucleotide sequence of a synthetic chimeric protein.
US-10-997-822-3

```

Query Match	64.5%	Score 60;	DB 9;	Length 276;
Best Local Similarity	57.6%	Pred. No. 8.2e-11;		
Matches 53; Conservative	19;	Mismatches 20;	Indels 0;	Gaps 0;

[illegible]

RESULT 11  
 US-10-997-700-75  
 : Sequence 75, Application US/10997700  
 : Publication No. US20050239172A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Wagnert, P.  
 : APPLICANT: peng, L.  
 : APPLICANT: Xia, U.  
 : APPLICANT: Holmquist, B.  
 : TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptide  
 : FILE REFERENCE: 1627.009US1  
 : CURRENT APPLICATION NUMBER: US/10/997,700  
 : CURRENT FILING DATE: 2004-11-24  
 : PRIOR APPLICATION NUMBER: US 60/383,212  
 : PRIOR FILING DATE: 2002-05-24

```

; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic PCR product.
; OS-10-997-700-75

```

Query Match	64.5%;	Score 60;	DB 9;	Length 276;
Best Local Similarity	57.6%;	Pred. No. 8.2e-11;		
Matches 53; Conservative	19;	Mismatches 20;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 12
US-10-997-078-133
; Sequence 133, Application US/10997078
; Publication No. US2005022144A1
GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptide
FILE REFERENCE: 1627.01USU1
CURRENT FILING DATE: 2004-11-24
PRIORITY APPLICATION NUMBER: US/10/997,078
PRIORITY FILING DATE: 2003-05-23
PRIORITY APPLICATION NUMBER: US 60/383,370
PRIORITY FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 133
LENGTH: 262
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: A synthetic sequence for the T7tagVg-PTH(1-34) cassette.
US-10-997-078-133

```

Query Match	64.5%	Score 60;	DB 9;	Length 282;
Best Local Similarity	57.6%	Pred. No. 8.2e-11;		
Matches 53; Conservative	19;	Mismatches 20;	Indels 0;	Gaps 0;

0y 2 CUGUUCGGAUUCUCCACUUAUCGACGUGUGUGUGUGUUCACUGAACCG 61  
 ||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::  
 Db 167 CUGTTTCGGAATCAGCTATGACACACCTGGGTAAACCTGAACCTTAGAAGCTG 226  
 0y 62 UUGAAUUGCUCGUAUAAAAACUGCAGACGACUU 93  
 ::||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::  
 Db 227 TTGAATGGCTCTCGTAAAAAATCGCAGAGCGTT 258

RESULT 13  
US-10-997-700-76  
Sequence 76, Application US/10997700  
Publication No. US20050239172A1  
GENERAL INFORMATION:  
APPLICANT: Magner, P.  
APPLICANT: Peng, L.  
APPLICANT: Xia, U.  
APPLICANT: Holmquist, B.

```

; TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptide
; FILE REFERENCE: 1627.009US1
; CURRENT APPLICATION NUMBER: US/10/997,700
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: US 60/383,212
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic PCR product.
; US-10-997-700-76
```

```

Query Match      64.5%; Score 60; DB 9; Length 291;
Best Local Similarity 57.6%; Pred. No. 8.3e-11;
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
```

```

Qy 2 CUGUUCGGAUAUCCAGCUGAUGCAGGUGUGUGUGUGUGUGUGUGUCCAUUGAAGUG 61
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 29 CTGTTTCGAAATCCAGCTGATGCACAACCTGGGTAACACCTGAACCTATGGAACGTG 88
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy 62 UUGAUGGCGUGUAAAAAACUGCAGACGCU 93
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 89 TTGAATGGCTGCTAAAAAACTGCAGACGTT 120
```

```

RESULT 14
US-10-997-700-77
; Sequence 77, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, F.
; APPLICANT: Peng, L.
; APPLICANT: Xia, U.
; APPLICANT: Holmquist, B.
; TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptide
; FILE REFERENCE: 1627.009US1
; CURRENT APPLICATION NUMBER: US/10/997,700
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: US 60/383,212
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic PCR product.
; US-10-997-700-77
```

```

Query Match      64.5%; Score 60; DB 9; Length 291;
Best Local Similarity 57.6%; Pred. No. 8.3e-11;
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
```

```

Qy 2 CUGUUCGGAUAUCCAGCUGAUGCAGGUGUGUGUGUGUGUGUGUCCAUUGAAGUG 61
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 29 CTGTTTCGAAATCCAGCTGATGCACAACCTGGGTAACACCTGAACCTATGGAACGTG 88
   ::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy 62 UUGAUGGCGUGUAAAAAACUGCAGACGCU 93
   ::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 89 TTGAATGGCTGCTAAAAAACTGCAGACGTT 120
```

```

RESULT 15
US-10-997-700-91
; Sequence 91, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, F.
```

```

; APPLICANT: Peng, L.
; APPLICANT: Xia, U.
; APPLICANT: Holmquist, B.
; TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptide
; FILE REFERENCE: 1627.009US1
; CURRENT APPLICATION NUMBER: US/10/997,700
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: US 60/383,212
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic pBN121-T7tag-CH-PTH (1-84).
; US-10-997-700-91
```

```

Query Match      64.5%; Score 60; DB 9; Length 321;
Best Local Similarity 57.6%; Pred. No. 8.5e-11;
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
```

```

Qy 2 CUGUUCGGAUAUCCAGCUGAUGCAGGUGUGUGUGUGUGUGUGUCCAUUGAAGUG 61
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 62 CTGTTTCGAAATCCAGCTGATGCACAACCTGGGTAACACCTGAACCTATGGAACGTG 121
   ::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy 62 UUGAUGGCGUGUAAAAAACUGCAGACGCU 93
   ::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 122 TTGAATGGCTGCTAAAAAACTGCAGACGTT 153
```

```

Search completed: November 24, 2005, 04:46:56
Job time : 413.667 secs
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```

? FILE REFERENCE: 821A
? CURRENT APPLICATION NUMBER: US/10/821.234
? CURRENT FILING DATE: 2004-04-07
? PRIOR APPLICATION NUMBER: US 60/462,047
? PRIOR FILING DATE: 2003-04-07
? NUMBER OF SEQ ID NOS: 1704
? SOFTWARE: pc_seq_genes Version 1.0
? SEQ ID NO 839
? LENGTH: 6497
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-10-821-234-839

```

[illegible]

```

RESULT 3
US-10-392-234A-15/c
Sequence 15, Application US/10392234A
Publication No. US20050255538A1
GENERAL INFORMATION:
APPLICANT: Pharmacia and Upjohn Corporation
APPLICANT: Buxser, Steven
APPLICANT: Poole, Keith
APPLICANT: Decker, Douglas
APPLICANT: Kiazad, Li
TITLE OF INVENTION: Method for Screening for AcrAB Transporter Family Inhibitors
FILE REFERENCE: 6206
CURRENT APPLICATION NUMBER: US/10/392,234A
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US 60/364,935
PRIOR FILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 3138
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-10-392-234A-15

```

Query March	26.0%;	Score 24.2;	DB 1;	Length 3138;
Best Local Similarity	50.7%;	Pred. No. 21;		
Matches 33;	Conservative	6;	Mismatches 28;	Indels 0;
			Gaps	0;
QY	23	UGCACGUGUGUGUGUGUGUGUCUUCATGCAACGUGUGAUGCGUGGAAAAAC	82	
Db	137	TGACGCGCGATGCGCGCGCGCGCGATGCGCGCGGATCTGCGTTGACCGCGAAGTGAAGATC	78	
QY	83	UGCAGAGACG	91	
Db	77	GACAGGCGG	69	

RESULT 4  
US-10-485-517-4  
Sequence 4, Application US/1048517  
Publication No. US20050256299A1  
GENERAL INFORMATION:  
APPLICANT: University of Sheffield  
APPLICANT: Biosynexus Incorporated  
APPLICANT: Foster, Simon  
TITLE OF INVENTION: Antigenic Polypeptides

```

; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-06-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 5690
;
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-485-517-4

```

[illegible]

```

RESULT 5
US-10-927-641-116/c
; Sequence 116, Application US/10927641
; Publication No. US20050244968A1
GENERAL INFORMATION:
APPLICANT: Pereira, Rantjan
APPLICANT: Rice, Stephen
APPLICANT: Eagleston, Clara
APPLICANT: Lasham, Annette
APPLICANT: Wood, Marion
APPLICANT: Visser, Elizabeth
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Expression
FILE REFERENCE: 11000.1036c4
CURRENT APPLICATION NUMBER: US/10/927,641
PRIOR FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/137,036
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/NZ00/00018
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 143
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 116
LENGTH: 947
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-10-927-641-116

```

	Query Match	25.2%;	Score 23.4;	DB 1;	Length 947;
	Best Local Similarity	51.2%;	Pred. No. 29;		
	Matches	21;	Mismatches	11;	Gaps 0;
Oy	26	ACGGGCGCGCCGCCGCCTCAGCAAGTTCATGTTTGGA	66		
Db	528	ATGGGTGCGGCGTGGGCGGTGCGGTGCGGTGCGGTGATAA	488		

```

RESULT 6
US-10-821-234-318
: Sequence 318, Application US/10821234
: Publication No. US20050255114A1
: GENERAL INFORMATION:
:   APPLICANT: Labat, Ivan
:   APPLICANT: Stache-Crain, Birgit
:   APPLICANT: Andarmani, Susan
:   APPLICANT: Tang, Y. Tom
: TITLE OR INVENTION: Methods for Diagnosis and Treatment of Pre-eclampsia
: FILE REFERENCE: 821A
: CURRENT APPLICATION NUMBER: US/10/821.234
: CURRENT FILING DATE: 2004-04-07
: PRIOR APPLICATION NUMBER: US 60/462,047
: PRIOR FILING DATE: 2003-04-07
: NUMBER OF SEQ ID NOS: 1704
: SOFTWARE: pc_seq_genes Version 1.0
: SEQ ID NO 318
:   LENGTH: 1657
:   TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-821-234-318

```

Query Match	25.2%	Score 23.4	DB 1	Length 1657
Best Local Similarity	54.4%	Pred. No. 33		
Matches	31	Conservative	5	Mismatches 21; Indels 0; Gaps 0;
Qy	5	UUUCCGAUAUCCAGUCAGUCAGUGUGUGUGUGUGUGUGUGUCUACAAGG	61	
Db	1231	TTTCGGAAGTCCATAGGAGCCCGCCGCGGAGAGGAGCCGCTGTGGACATGGGCCCCG	1287	

```

RESULT 7
US-10-821-234-255/c
? Sequence 255: Application US/10821234
? Publication No. US200502551141
? GENERAL INFORMATION:
? APPLICANT: Labat, Ivan
? APPLICANT: Stache-Crain, Birgit
? APPLICANT: Andarmani, Susan
? APPLICANT: Tang, Y. Tom
? TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
? FILE REFERENCE: 821A
? CURRENT APPLICATION NUMBER: US/10/821,234
? CURRENT FILING DATE: 2004-04-07
? PRIOR APPLICATION NUMBER: US 60/462,047
? PRIOR FILING DATE: 2003-04-07
? NUMBER OF SEQ ID NOS: 1704
? SOFTWARE: pc_seq_genes Version 1.0
? SEQ ID NO 255
? LENGTH: 3893
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-821-234-255

```

Query Match	Similarity	Score	23.2	DB 1	Length	3893
Best Local	Similarity	43.2%	Pred. No. 47			
Matches	19	Conservative	12	Mismatches	13	Indels
					0	Gaps
						0
Qy	5	UUUCCGAUUAUCCAGCUGAUU	GCAGCUGUGUGUGUGUGUGUGU	48		
Db	2665	TTTCGGAGGTGATGATGATGATG	ATGATGATGATGATGATGATGATG	2622		

RESULT 8  
US-10-509-422-1/c  
Sequence 1, Application US/10509422  
Publication No. US20050244825A1  
GENERAL INFORMATION:  
APPLICANT: Liou, Simon  
TITLE OF INVENTION: Human BMP2 Inducible Kinases

```

1 FILE REFERENCE: 004974.01015
2
3 CURRENT APPLICATION NUMBER: US/10/509,422
4
5 CURRENT FILING DATE: 2004-09-24
6
7 PRIOR APPLICATION NUMBER: PCT/EP03/080825
8
9 PRIOR FILING DATE: 2003-03-20
10
11 PRIOR APPLICATION NUMBER: US 60/367,512
12
13 PRIOR FILING DATE: 2002-03-27
14
15 PRIOR APPLICATION NUMBER: US 60/406,936
16
17 PRIOR FILING DATE: 2002-08-30
18
19 NUMBER OF SEQ ID NOS: 9
20
21 SOFTWARE: FastSeq for Windows Version 4.0
22
23 SEQ ID NO 1
24
25     LENGTH: 3507
26
27     TYPE: DNA
28
29     ORGANISM: Homo sapiens
30
31 US-10-509-422-1

```

		Query Match	24.7%; Score 23; DB 1; Length 3507;
		Best Local Similarity	46.8%; Pred. No. 53;
		Matches	22; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
QY	2	CCTGTCGGAAATCCAGTCAUACGCGUGUGUGUGUGUGUGU	48
		:   :   :   :   :   :   :   :   :   :   :   :   :	
DB	1509	CCTGCTGATATTACGATCTTGAACTAGGTGGTGGTGGTGGTGGT	1463

```

RESULT 9
US-10-509-422-3/c
; Sequence 3, Application US/10509422
; Publication No. US20050244825A1
; GENERAL INFORMATION:
; APPLICANT: Lion, Simon
; TITLE OF INVENTION: Human BMP2 Inducible Kinases
; FILE REFERENCE: 004974.01015
; CURRENT APPLICATION NUMBER: US/10/509,422
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: PCT/EP03/080825
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/367,512
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/406,936
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3704
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-509-422-3

```

Query Match Similarity 24.7%; Score 23; DB 1; Length 3704;  
Beet Local Similarity 46.8%; Pred. No. 54;  
Matches 22; Conservative 10; Mismatches 15; Indels 0; Gaps 0.

RESULT 10  
US-11-005-030-1/C  
; Sequence 1, Application US/11005030  
; Publication No. US2005025495A1  
; GENERAL INFORMATION:  
; APPLICANT: Aerssens, Jercoen  
; APPLICANT: Athanasios, Maria  
; APPLICANT: Brain, Carlos  
; APPLICANT: Cohen, Nadine  
; APPLICANT: Dain, Bradley  
; APPLICANT: Denton, R. Rex  
; APPLICANT: Judson, Richard S.  
; APPLICANT: Ozdemir, Vural  
; APPLICANT: Reed, Carol R.

```

TITLE OF INVENTION: SLCS5A7 Genetic Markers Associated with Age of Onset of
TITLE OF INVENTION: Alzheimer's Disease
FILE REFERENCE: 2300.0090001
CURRENT APPLICATION NUMBER: US/11/005,030
CURRENT FILING DATE: 2004-12-07
PRIORITY APPLICATION NUMBER: US 60/529,999
PRIORITY FILING DATE: 2003-12-15
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.3
SEQ ID NO. 1
LENGTH: 26323
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1973)..(1973)
OTHER INFORMATION: n is 'g' or 'a'
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2010)..(2010)
OTHER INFORMATION: n is 't' or 'c'
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2273)..(2273)
OTHER INFORMATION: n is 'a' or 'g'
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2417)..(2417)
OTHER INFORMATION: n is 't' or 'c'
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7671)..(7671)
OTHER INFORMATION: n is 'g' or 't'
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16520)..(16520)
OTHER INFORMATION: n is 'c' or 't'
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16546)..(16546)
OTHER INFORMATION: n is 'g' or 'a'
US-11-005-030-1
Query Match 24.7%; Score 23; DB 7; Length 26323;
Best Local Similarity 47.9%; Pred. No. 83;
Matches 34; Conservative 7; Mismatches 30; Indels 0; Gaps 0;
QY 19 CUGAUGCAGCGUGUGUGUGUGUGUGUGUCCAUAGAACGUGUGAUGCGUCGUA 78
Db 23951 CUGGAGCCGUGTGGGGGCGTGGGGGCGTGCAGGAAGAACTTAGAGCAGGCTCA 23892
QY 79 AAACUGCAGGA 89
Db 23891 TAGGTGCAGCA 23881
RESULT 11
US-10-667-295-44/C
Sequence 44. Application US/10667295
Publication No. US20050257293A1
GENERAL INFORMATION:
APPLICANT: Macelis, Peter
TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REFERENCE: 11696-047001
CURRENT APPLICATION NUMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
PRIORITY APPLICATION NUMBER: US 60/411,823
PRIORITY FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 263
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 44
LENGTH: 481
TYPE: DNA

```

```

; ORGANISM Brassica napus ;
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(481)
; OTHER INFORMATION: Ceres Seq. ID no. 6425497
US-10-667-295-44

Query Match          24.3% Score 22.6; DB 1; Length 481;
Best Local Similarity 41.5%; Pred. No. 46;
Matches 22; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

OY      25 CACGGUGUGUGUGUGUGUGUGUGUCCAGAACGUGUGAUGCUCGCUAA 77
Db      399 CACTGGATTCCTTGAGTGTGTTGCATGAATAATTCAATGAGCGCCTCAA 347
|||||..||..||..||..||..||..||..||..||..||..||..||..||..||..||

RESULT 12
US-10-821-234-119/c
; Sequence 119, Application US/10821234
; Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labac, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmant, Suneau
APPLICANT: Teng, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIORITY FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_seq_genes Version 1.0
SEQ ID NO 119
LENGTH: 2218
TYPE: DNA
ORGANISM: Homo sapiens
US-10-821-234-119

Query Match          24.3% Score 22.6; DB 1; Length 2218;
Best Local Similarity 51.4%; Pred. No. 65;
Matches 19; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

OY      28 GGUGUGUGUGUGUGUGUGUGUUCCAUGAACGUGUG 64
Db      1753 GGUGUGUGUGUGUGUGUGUGTTGAGACAGGTCCTCGTTG 1717
|||||..||..||..||..||..||..||..||..||..||..||..||..||..||..||

RESULT 13
US-10-509-921-9/c
; Sequence 9, Application US/10509921
; Publication No. US20050250093A1
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham Corporation
TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
FILE REFERENCE: P51335
CURRENT APPLICATION NUMBER: US/10/509,921
CURRENT FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: 60/369,685
PRIORITY FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 7979
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Thepoly nucleotide sequence encodes sequences from
US-10-509-921-9

Query Match          24.3% Score 22.6; DB 1; Length 7979;
Best Local Similarity 43.5%; Pred. No. 86;

```

Matches 30; Conservative 10; Mismatches 29; Indels 0; Gaps 0;  
QY 2 CUGUUUCCGAUAUCCAGCUGACGUGUGUGUGUGUGUGUCCAUAGAAACGUG 61  
Db 5734 CTGTCAAGACAAACCGCTCTTCTCCGTGAGGTGATTGAGAGACCTTGGTAGGTG 5675  
QY 62 UUGAUGGC 70  
Db 5674 GCAATGGGC 5666

## RESULT 14

US-10-509-921-10/c  
; Sequence 10, Application US/10509921  
; Publication No. US20050250093A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Corporation  
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons  
; FILE REFERENCE: P51335  
; CURRENT APPLICATION NUMBER: US/10/509,921  
; CURRENT FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER: 60/369,685  
; PRIOR FILING DATE: 2002-04-03  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PasteSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 7979  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from  
; OTHER INFORMATION: HCV J4(U4B/R1(C))Replicons  
US-10-509-921-10

Query March 24.3%; Score 22.6; DB 1; Length 7979;  
Best Local Similarity 43.5%; Pred. No. 86;  
Matches 30; Conservative 10; Mismatches 29; Indels 0; Gaps 0;

QY 2 CUGUUUCCGAUAUCCAGCUGACGUGUGUGUGUGUGUCCAUAGAAACGUG 61  
Db 5734 CTGTCAAGACAAACCGCTCTTCTCCGTGAGGTGATTGAGAGACCTTGGTAGGTG 5675  
QY 62 UUGAUGGC 70  
Db 5674 GCAATGGGC 5666

## RESULT 15

US-10-509-921-11/c  
; Sequence 11, Application US/10509921  
; Publication No. US20050250093A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Corporation  
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons  
; FILE REFERENCE: P51335  
; CURRENT APPLICATION NUMBER: US/10/509,921  
; CURRENT FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER: 60/369,685  
; PRIOR FILING DATE: 2002-04-03  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PasteSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 7979  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from  
; OTHER INFORMATION: HCV J4 Replicons  
US-10-509-921-11

Query March 24.3%; Score 22.6; DB 1; Length 7979;  
Best Local Similarity 43.5%; Pred. No. 86;  
Matches 30; Conservative 10; Mismatches 29; Indels 0; Gaps 0;

QY 2 CUGUUUCCGAUAUCCAGCUGACGUGUGUGUGUGUGUCCAUAGAAACGUG 61  
Db 5734 CTGTCAAGACAAACCGCTCTTCTCCGTGAGGTGATTGAGAGACCTTGGTAGGTG 5675  
QY 62 UUGAUGGC 70  
Db 5674 GCAATGGGC 5666

Search completed: November 24, 2005, 04:56:48  
Job time : 196 secs

Page 10 of 10  
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Result No.	Score	Query Match	Length	DB	ID	Description
1	93	100.0	93	6	BD266834	BD266834 PTH funct
2	73.8	79.4	93	6	BD266832	BD266832 PTH funct
3	64.2	69.0	93	6	BD266833	BD266833 PTH funct
4	53.6	57.6	258	6	AR2659042	AR2659042 Sequence
5	48.4	52.0	74	6	AR043802	AR043802 Sequence
C	46.2	49.7	141	6	AR005132	AR005132 Sequence
C	46.2	49.7	141	6	AR005133	AR005133 Sequence
C	46.2	49.7	141	6	AR177779	AR177779 Sequence
8	46.2	49.7	141	6	AR177780	AR177780 Sequence
9	46.2	49.7	141	6	AR043797	AR043797 Sequence
C	46.2	49.7	207	6	AS6847	AS6847 Sequence 1
10	46.2	49.7	717	6	A36849	A36849 Sequence 3
11	44.6	48.0	945	6	BD234383	BD234383 Recombina
12	44.6	48.0	945	6	BD234385	BD234385 Recombina
13	44.6	48.0	945	6	BD234386	BD234386 Recombina
14	44.6	48.0	945	6	BD234384	BD234384 Recombina
15	44.6	48.0	945	6	BD234390	BD234390 Recombina
16	44.6	48.0	945	6	BD234387	BD234387 Recombina
17	44.6	48.0	945	6	BD234388	BD234388 Recombina
18	44.6	48.0	945	6	BD234389	BD234389 Recombina

19	44	47.3	423	6	BD234388	BD234388 Recombina
20	44	46.7	435	6	BD234389	BD234389 Recombina
21	43.4	46.3	45	6	BD073301	BD073301 Recombina
22	43.4	46.7	45	6	AR269023	AR269023 Sequence
23	43	46.2	67	6	A79761	A79761 Sequence 9
24	43	46.5	67	6	AR135774	AR135774 Sequence
25	41.4	44.2	71	6	BD234410	BD234410 Recombina
26	39.8	42.8	224	6	AR027007	AR027007 Sequence
27	39.8	42.8	234	6	AR027049	AR027049 Sequence
28	39.8	42.8	234	6	E05661	E05661 DNA encodin
29	39.8	42.8	234	6	E05676	E05676 DNA encodin
30	39.8	42.8	237	6	AR027008	AR027008 Sequence
31	39.8	42.8	237	6	E05662	E05662 DNA encodin
32	39.8	42.8	240	6	AR027009	AR027009 Sequence
33	39.8	42.8	240	6	E05663	E05663 DNA encodin
34	39.8	42.8	243	6	AR027010	AR027010 Sequence
35	39.8	42.8	243	6	E05664	E05664 DNA encodin
36	39.8	42.8	245	6	AR027012	AR027012 Sequence
37	39.8	42.8	245	6	E05659	E05659 DNA encodin
38	39.8	42.8	247	6	AR027013	AR027013 Sequence
39	39.8	42.8	247	6	E05660	E05660 DNA encodin
40	39.8	42.8	248	6	AR027014	AR027014 Sequence
41	39.8	42.8	248	6	E05665	E05665 DNA encodin
42	39.8	42.8	250	6	AR027015	AR027015 Sequence
43	39.8	42.8	250	6	E05666	E05666 DNA encodin
44	39.8	42.8	251	6	AR027016	AR027016 Sequence
45	39.8	42.8	251	6	E05667	E05667 DNA encodin

## ALIGNMENTS

RESULT 1	BD266834	93 bp RNA	linear	PAT 17-JUL-2003
LOCUS	BD266834			
DEFINITION	PMH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules.			
ACCESSION	BD266834.1	GI:33076602		
VERSION	UP 200253115-A/3.			
KEYWORDS	synthetic construct			
SOURCE	other sequences; artificial			
ORGANISM	synthetic construct			
REFERENCE	1. (bases 1 to 93)			
AUTHORS	Gaddella,T.D., Kronenberg,H.M., Potts,J.T. and Jueppner,H.			
TITLE	PMH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules			
JOURNAL	Patent: JP 200253115-A 3 08-OCT-2002;			
COMMENT	THE GENERAL HOSPITAL CORP			
	OS	Artificial Sequence		

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PC A61P31/10,PC
PC A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19,PC
PC C12N1/21,PC
PC C12N5/10,C01N33/15,C01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
Description of Artificial Sequence: modified PTH sequence FH Key
Location/Qualifiers
1. .93
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FT

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**FEATURES**  
**source**

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ORIGIN

Query Match	100.0%;	Score 93;	DB 6;	Length 93;
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	Best Local Similarity	72.0%; Pred. No. 1.5e-16; Matches 67; Conservative 26; Mismatches 0; Indels 0; Gaps 0;
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Dd	61 GTTGAATGCCGTGCTGTAATAAACTGCAGACCTT 93	
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LOCUS	BD266832	
DEFINITION	PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules.	
ACCESSION	BD266832.1	GI:33076600
VERSION	JP 2002533115-A/1.	
KEYWORDS	synthetic construct	
ORGANISM	other sequences; artificial sequences.	
REFERENCE	1 (bases 1 to 93)	
AUTHORS	Gardella,T.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.	
TITLE	PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules	
JOURNAL	Patent: JP 2002533115-A 1 08-OCT-2002; THE GENERAL HOSPITAL CORP	
COMMENT	OS Artificial Sequence PN JP 2002533115-A/1 PD 08-OCT-2002 PP 30-DEC-1999 JP 2000591171 PR 31-DEC-1998 US 60/114577 PI THOMAS J GARDELLA,HENRY M KRONENBERG,JOHN T POTTS,HAROLD PI JUEPPNER PC C12N15/09,A61K38/00,A61K5/00,A61K48/00,A61P5/18,A61P19/08, PC A61P19/10 PC A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC C12N1/21, PC C12N5/10,G01N33/15,G01N33/50,C12M5/00,C12M5/00,A61K37/02 CC Description of Artificial Sequence: modified PTH sequence FH Key	
FEATURES	FT source Location/Qualifiers FT 1..93 Location/Qualifiers 1..93 Location/Qualifiers 1..93 /organism='Artificial Sequence'. /organism='Synthetic Construct' /mol_type='genomic RNA' /db_xref='taxon:32630'	
ORIGIN	Query Match 79.4%; Score 73.8; DB 6; Length 93; Best Local Similarity 63.4%; Pred. No. 6e-11; Matches 59; Conservative 22; Mismatches 12; Indels 0; Gaps 0;	
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Dd	61 GTTGAATGCCGTGCTGTAATAAACTGCAGACCTT 93	
Oy	61 GTTGAATGCCGTGCTGTAATAAACTGCAGACCTT 93	
RESULT 3	BD266833	93 bp RNA linear PAT 17-JUL-2003
LOCUS	BD266833	
DEFINITION	PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules.	
ACCESSION	BD266833	GI:33076601
KEYWORDS	JP 2002533115-A/2.	

[illegible]



[illegible][illegible]



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ORIGIN

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QY      62  UUGAUGGCUCCGUAAAAAACUGCAGAGACGU  92
      : |||:||||:||||:||||:||||:| :
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RESULT 13			
BD234383			
LOCUS	BD234383	405 bp	DNA linear
DEFINITION	Recombinant synthesis of beta-lipotropin and other peptides.		

SOURCE ORGANISM	synthetic construct synthetic construct other sequences; artificial sequences
-----------------	---

**AUTHORS** Hale, J. E., Herzberger, C. L., Larson, J. L. and Menke, M. A.  
**TITLE** Recombinant synthesis of beta-1ipotrogin and other peptides  
**JOURNAL** Patent: JP 2002533072-A 4 08-OCT-2002;

COMMENT	OS Artificial Sequence
	PN JP 2002533072-A/4

ED	15-DEC-1998	JP	2000589671
PD	21-DEC-1998	US	60/113058
PR	JOHN EDWARD HALE, CHARLES LEE HERSHBARGER, JEFFREY LYNN LARSON		
PI	MICHAEL ANDREW MENKE		
PC	C12M15/09, C07K14/67, C07K19/00, C12N1/15, C12N1/19, C12N1/21		
PC	C12N5/10, C12N9/50,		
PC	C12B21/02, C12M15/00, C12N5/00		
CC	Description of Artificial Sequence: PCGB-RVR-hPTH fusion		
Key	Location/Qualifiers		
FT	CDS	(4)	. (393)

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Best Local Similarity	47.8%	Pred. No. 0.029		
Matches 44;	Conservative	18;	Mismatches 30;	Indels 0;
			Gaps	0

[illegible]

**OY**      62 UUGAAUUGCUCGCGUAAAAACUGCAGACGUU 93  
         : |||:|||:|||:|||:|||:|||:::  
**Db**      353 TAGAATGGCTGCGTAGAAGCTGCAGATGTT 384

RESULT 14	BD234385	408 bp	DNA linear	PAT 17-JUL-2003
LOCUS	BD234385			
DEFINITION	Recombinant synthesis of beta-lipotropin and other peptides.			
ACCESSION	BD234385			
VERSION	BD234385.1	GI:3304155		
KEYWORDS	JP 2002533072-A/6.			
SOURCE	synthetic construct			
ORGANISM	synthetic construct			

## REFERENCE

**AUTHORS** Hale, J.E., Hershenberger, C.L., Larson, J.L. and Menke, M.A.  
**TITLE** Recombinant synthesis of beta-lipotropin and other peptides  
**JOURNAL** Patent: JP 2002533072-A 6 08-OCT-2002;  
INTERNET AND CO.

**COMMENT**

PD	08-OCT-2002	JP	2000589671
PF	15-DEC-1999	US	60/113058
PR	21-DEC-1998	US	60/113058
PI	JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON		
PI	MICHAEL ANDREW MENKE		
PC	C12N15/09, C07K14/67, C07K19/00, C12N1/15, C12N1/19, C12N1/21	PC	
	, C12N5/10, C12N9/50,		
	PC C12P21/02, C12N15/00, C12N5/00		
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Key	Location/Qualifiers		
FT	CDS (4) . . (396) .		

FEATURES

SOURCE

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**ORIGIN**

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 Db 296 ctgttttcgaatctcagctgatgcattacctggcgaaacacttgaaacttatggagcgtg    355

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Db      356 TAGAATGGCTGCGCTAAGAAAGCTGCAGGATGTT  38
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## RESULT 15

LOCUS	408 bp	DNA	linear	PAT 17-JUL-2003
BD534386				
DEFINITION	Recombinant synthesis of beta-lipotropin and other peptides.			
REMARKS	n003120c			

VERSION BD234386.1 GI:33044156  
KEYWORDS JP 2002533072-A/7.  
SOURCE synthetic construct  
ORIGIN synthetic construct

ORGANISM	SYNTHETIC CONSTRUCT
1 (bases 1 to 408)	other sequences; artificial sequences

REFERENCE	1 (bases 1 to 498)
AUTHORS	Hale, J.E., Herschberger, C.L., Larson, J.L. and Menke, M.A.
TITLE	Recombinant synthesis of beta-1ipoprotein and other peptides
JOURNAL	Patent: JP 2002533072-A 7 08-OCT-2002;
COMMENT	ELI LILLY AND CO
OS	Artificial Sequence
DI	Artificial Sequence

COMMENT

PD 08-OCT-2002  
PD 15-DEC-1999 JP 2000589671  
PR 21-DEC-1998 US 60/113058  
PI JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON,  
PI MICHAEL ANDREW MENKE  
PC C12N5/09, C07K14/67, C07K19/00, C12N1/15, C12N1/79, C12N1/21 PC  
PC C12N5/10, C12N9/50,  
PC C12P21/02, C12N15/00, C12N5/00



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:00:32 ; Search time 242.667 Seconds  
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2554.189 Million cell updates/sec

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Listing first 45 summaries

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5: geneseq2001bs:\*  
6: geneseq2002as:\*  
7: geneseq2002bs:\*  
8: geneseq2003as:\*  
9: geneseq2003bs:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	93	100.0	93	3	AAA51731	AAA51731 PTH funct
2	73.8	79.4	93	3	AAA51729	AAA51729 PTH funct
3	64.2	69.0	93	3	AAA51730	AAA51730 PTH funct
4	52	55.9	152	2	AAT73910	AAT73910 Synthetic
5	52	55.9	489	12	ADG48030	ADG48030 Human PTH
6	52	55.9	489	12	ADG48059	ADG48059 Human PTH
7	52	55.9	489	12	ADG68786	ADG68786 Human mut
8	50.4	54.2	102	12	ADG93179	ADG93179 Novel exp
9	50.4	54.2	102	12	ADG65857	ADG65857 PTH pepti
10	50.4	54.2	102	12	ADW14377	ADW14377 Human par
11	50.4	54.2	111	12	ADG93180	ADG93180 Novel exp
12	50.4	54.2	111	12	ADJ65858	ADJ65858 PTH pepti
13	50.4	54.2	111	13	ADW14375	ADW14375 Human par
14	50.4	54.2	117	12	ADG93260	ADG93260 Novel exp
15	50.4	54.2	168	2	AAT34865	AAT34865 Plasmid p
16	50.4	54.2	252	12	ADG93181	ADG93181 Novel exp
17	50.4	54.2	252	12	ADJ65859	ADJ65859 PTH prote
18	50.4	54.2	264	12	ADJ65913	ADJ65913 Tandem po
19	50.4	54.2	276	12	ADP90345	ADP90345 Chimeric

20	50.4	54.2	276	12	ADJ65899	ADJ65899 PTH DNA s
21	50.4	54.2	276	12	ADJ87051	ADJ87051 Nucleotid
22	50.4	54.2	282	12	ADG93252	ADG93252 Novel exp
23	50.4	54.2	291	12	ADJ65901	ADJ65901 PTH DNA s
24	50.4	54.2	291	12	ADJ65900	ADJ65900 PTH DNA s
25	50.4	54.2	294	2	AAT34866	AAT34866 Plasmid p
26	50.4	54.2	321	12	ADJ65915	ADJ65915 Tandem po
27	50.4	54.2	420	12	ADJ65917	ADJ65917 Tandem po
28	50.4	54.2	420	12	ADP90347	ADP90347 Chimeric
29	50.4	54.2	426	12	ADP90347	ADP90347 Chimeric
30	49.4	53.1	528	6	AA519702	AA519702 DNA encod
31	49.4	53.1	108	13	ADV69494	ADV69494 Human par
32	46.4	49.9	52	13	ADV69502	ADV69502 Human par
33	46.2	49.7	141	2	AAO89920	AAO89920 Recombina
34	46.2	49.7	141	2	AAT80383	AAT80383 rPTH codi
35	46.2	49.7	207	2	AAO89923	AAO89923 Expressio
36	45.2	48.6	145	13	ADW80822	ADW80822 DNA encod
37	44.6	48.0	76	12	ADO42786	ADO42786 Human PTH
38	44.6	48.0	728	2	AAO55301	AAO55301 Truncated
39	44.6	48.0	945	2	AAO55302	AAO55302 gp55-Abn-
40	44.6	47.3	405	3	AA51452	AA51452 PCPB-LVPR
41	44.4	47.3	408	3	AA51455	AA51455 PCPB-LVPR
42	44.4	47.3	408	3	AA51454	AA51454 PCPB-LEGR
43	44.4	47.3	411	3	AA51453	AA51453 PCPB-ALY-
44	44.4	47.3	414	3	AA51459	AA51459 PCPB-APR-
45	44.4	47.3	417	3	AA51456	AA51456 PCPB-VIPR

# ALIGNMENTS

RESULT 1	
AA51731	AA51731 standard; RNA; 93 BP.
XX	
AC	AA51731;
XX	
DT	31-OCT-2000 (first entry)
XX	
DE	PTH functional domain conjugate peptide PG9 coding sequence.
XX	
KW	PTH: parathyroid hormone; conjugate; bone mass; bone reformation;
KW	resorption; remodeling; tether1; osteoporosis; ss.
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OS	Homo sapiens.
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OS	Synthetic.
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PH	Location/Qualifiers
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XX	
PD	06-JUL-2000.
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PF	30-DEC-1999; 99WO-US031108.
XX	
PR	31-DEC-1998; 98US-0114577P.
XX	
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PA	(KRON/) KRONENBERG H M.
PA	(POTT/) POTTS J T.
PA	(JUEP/) JUEPPNER H.
XX	
PI	Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX	
DR	WPI: 2000-452384/39.
XX	
DR	P-PSDB; AAY96974.
XX	
PT	New compound comprising an amino terminal signaling functional domain
PT	linked to a carboxy-terminal binding portion of parathyroid hormone for
PT	treating mammalian conditions characterized by decreases in bone mass.



PA (BOEF ) BOEHRINGER MANNHEIM GMBH

PF 03-APR-2003; 2003US-00407078.





[illegible]

DR		WPI : 2004-035128/03.
DR	P-PsDB; ADG93159.	
XX	New expression cassette comprising an operably linked nucleic acid	
PT	sequence, useful for producing a tandem polypeptide that forms an	
PT	inclusion body when expressed in a cell.	
XX		
PS	Disclosure; SEQ ID NO 60; 157pp; English.	
CC		
XX	This invention relates to a novel expression cassette and methods for	
CC	high yield production of polypeptides. The cassette comprises an operably	
CC	linked nucleic acid sequence, where the expression of the cassette	
CC	produces a tandem polypeptide that forms an inclusion body when expressed	
CC	in a cell. The expression cassette is useful for producing peptide and	
CC	polypeptide in a cell, preferably a tandem polypeptide that forms an	
CC	inclusion body when expressed in a cell. The present sequence is that of	
CC	a DNA sequence which encodes a polypeptide which may be produced using	
CC	the expression cassette of the invention.	
XX		
SQ	Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;	
	Query Match 54.2%; Score 50.4; DB 12; Length 102;	
	Best Local Similarity 52.2%; Pred.No.5.le-06;	
	Matches 48; Conservative 18; Mismatches 26; Indels 0; Gaps 0	
Oy	. 2 CUGUUUCCGAACCGUGUGUGUGUGUGUGUGUCUCAACUCCAGAACGUG 61 :: ::   :: :	
Dd	2 CTGTTCCTGAATCCAGCTGCATGCACAACCTGGGTAAACACTTATGAAACGTG 61 :: ::   :: :	
Oy	62 UUGAUGCUGCUGAAAAAACUCGACGACGU 93 :: ::   :: :	
Dd	62 TTGAATGGCTGCTAAAATAACTGCACGACGTT 93 :: ::   :: :	
RESULT 9		
ID	ADJ65857 standard; DNA; 102 BP.	
XX	ADJ65857;	
AC		
XX	ADJ65857;	
DT	06-MAY-2004 (first entry)	
DE	PTH peptide coding sequence #1.	
XX		
XX	expression cassette; tandem polypeptide; inclusion body;	
KM	inclusion body fusion partner; PTH; gene; ds.	
XX		
OS	Unidentified.	
PN	WO2003j00022-A2.	
PD		
XX	04-DEC-2003.	
PF	23-MAY-2003; 2003WO-USO16645.	
PR		
PA	24-MAY-2002; 2002US-0383212P.	
(REST -)	RECTORAGEN INC.	
EI	Xia Y, Peng L;	
DR	WPI; 2004-035129/03.	
DR	P-PsDB; ADJ65837.	
PT	New expression cassette comprising an operably linked nucleic acid	
PT	sequence, useful for producing a tandem polypeptide that forms an	
XX	inclusion body when expressed in a cell.	
XX		
PS	Disclosure; SEQ ID NO 33; 132pp; English.	
CC	The invention comprises an expression cassette which produces a tandem	
CC	polypeptide that form an inclusion body when expressed in a cell. The	
CC	expression cassette of the invention is useful for producing a peptide or	



[illegible][illegible]

CC produces a tandem polypeptide that forms an inclusion body when expressed  
CC in a cell. The expression cassette is useful for producing peptide and  
CC polypeptide in a cell, preferably a tandem polypeptide that forms an  
CC inclusion body when expressed in a cell. The present sequence is that of  
CC a DNA sequence which encodes a PTH peptide which was used in the  
CC exemplification of the invention.

SQ Sequence 117 BP; 35 A; 27 C; 25 G; 30 T; 0 U; 0 Other;

Query Match	54.2%;	Score 50.4;	DB 12;	Length 117;
Best Local Similarity	52.2%;	Pred. No. 5.3e-06;		
Matches 48;	Conservative 18;	Mismatches 26;	Indels 0;	Gaps 0;

QY 2 CUGUUUCCGAAAUCCGUGUGUGUGUGUGUGUGUCUGAUCUCCAGGAACUG 61

Db 2 CTGTTCGAATCCAGCTGATGCACAACCTGGTAACAACCTGAACCTTATGGAACGTG 61

QY	62	TUGAUGCUCGCGUAAAAACUGCAGACGUT	93
	:	:     :     :     :	:
Db	62	TTGAATGGCTGCGTAAAAAACTGCAGACGTT	93

RESULT 15  
AAT34865

ID AAT34865 standard; cDNA; 168 BP.

AA AT34865; AC

DT 02-DEC-1996 (first entry)

Plasmid pBN1: PTH(1-34)C-1c portion encoding PTH(1-34)Cys.

AA PTH; parathyroid hormone; parathormone; C-amide; C-amidated peptide;  
KW alpha-carboxamide; recombinant protein; fusion protein; transpeptidation;  
KW vector; plasmid pBN1; carbonic anhydrase II; ss.

OS Synthetic.

XX	Location/Qualifiers
FH	1..162
FT	/*tag= a
CDS	/product= "hca-linker-PTH(1-34)Cys fusion"
FT	

PN WO9617941-A2.

PD 13-JUN-1996.

PF 07-DEC-1995; 95WO-US015799.

PR 07-DEC-1994; 94US-00350528.

PA (BION-) BIONEBRASKA INC.

Stout JS, Patridge BE, Heriksen DB, Holmquist B, Wagner FW;

WPI; 1996-287185/29.

XX  
XX

PT and transpeptidation of recombinant multicopy peptide(s) or fusion by creating a C-terminal alpha-carboxamidated peptide(s)

Example 7; Fig 1; 93pp; English.

A portion (AA1734865) of plasmid pBN1:PTH(1-134)-C-1c comprises DNA coding for a fusion protein (AA487867) composed of the C-terminal end of human chromatin acetyltransferase II joined by an intrconnecting peptide (including chromatin cleavage site) to amino acids 1-34 of PTH (AA989566), followed by a Cys residue and C-terminal sequence. The complete construct can be expressed in *E. coli* transformants. The intrconnecting peptide and C-terminal Cys residue enable the recombinant protein construct to be selectively reacted to produce C-terminal carboxamidated PTH(1-34).

Sequence 168 BP; 41 A; 44 C; 42 G; 41 T; 0 U; 0 Other;

Query Match 54.2%; Score 50.4; DB 2; Length 168;  
Best Local Similarity 52.2%; Pred. No. 5.7e-06;  
Matches 48; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

**DY**

| : | : | : | :

2 CUGUUUCCCAAUUCGUGUGUGUGUGUGUGUGUGUGAACCUCACUCCAUGCAGCUG 61  
||:::||::||:

**Db**

47 CTGTTCCTGAATCATCGACTGATGCACAACCTGGTGTAACAACCTTATTGNACTGTG 106

**Dy**      62 UUGAUGCUCGUAAAAACUGCAGACGCU 93  
          ::|::|::|::|::|::|::|::|::|::|:  
**Db**      107 TTGGATGCGCTGTAAAACCTGCAGACGTT 138

Search completed: November 23, 2005, 23:00:15  
Job time : 243.667 secs

Job time : 243.667 sec

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:36:53 ; Search time 1823 Seconds  
(without alignments)  
2386.834 Million cell updates/sec

Title: US-09-475-158A-16  
Perfect score: 1 gcuuuuuccgaauucgugug.....guaaaaaacgacgacguu 93  
Sequence: 93

Scoring table: IDENTITY NUC  
Gapop 10'-0', Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_est4.\*  
5: gb\_est5.\*  
6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_est9.\*  
10: gb\_est10.\*  
11: gb\_est11.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39.2	42.2	527	1	A1909008 QV-BT197-
2	38.8	41.7	324	8	W19763 AB99001.r1
3	38.2	41.1	352	8	W39062 ZB34C06.r1
4	38.2	41.1	376	8	W38966 ZB28D12.r1
5	38.2	41.1	411	8	W37708 ZC10D12.r1
6	38.2	41.1	416	8	W31998 ZB96D06.r1
7	38.2	41.1	434	8	W38764 ZB27A07.r1
8	38.2	41.1	450	8	W56235 ZC01E11.r1
9	38.2	41.1	453	8	W33077 ZC07A12.r1
10	38.2	41.1	496	8	W56820 ZC01A03.r1
11	38.2	41.1	523	8	W52945 ZC03H08.r1
12	38.2	41.1	536	8	W19765 ZB39C03.r1
13	38.2	41.1	547	8	W52795 ZC02B12.r1
14	38.2	41.1	578	8	W56120 ZC05H06.r1
15	38.2	41.1	583	8	W39202 ZB35H03.r1
16	38.2	41.1	595	1	AA788985 AB29C05.8
17	38.2	41.1	721	2	BG198564 RST17829
18	38.2	41.1	741	1	AI051997 CY29C05.x
19	38.2	41.1	756	1	AA843660 AK08G07.s
20	38.2	41.1	757	5	BX106232 BX106232
21	38.2	41.1	780	1	AI028087 CW51A12.x
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23	38.2	41.1	820	5	BX103059	BX103059 BX103059
24	37.2	40.0	316	1	AA372113	AA372113 EST83976
25	36.6	39.4	575	1	AA772070	AA772070 A141E07.s
26	36.6	39.4	620	6	CF231132	CF231132 Prac0017G
27	36.6	39.4	766	1	AA843141	AA843141 AK06C02.8
28	36.2	38.9	339	8	T29548	T29548 EST83988.Hu
29	35.8	38.5	844	6	CA184654	CA184654 SCLST316
30	35.6	38.3	417	9	CC894877	CC894877 ZMMBB021
31	35.6	38.3	570	1	AA771739	AA771739 A132E09.s
32	35.4	38.1	605	7	CO964533	CO964533 GM89013B2
33	35	37.6	540	2	BE212803	BE212803 IPBrt0085
34	35	37.6	705	1	AI031553	AI031553 ow48C08.x
35	34.8	37.4	301	11	CR159040	CR159040 Forward.s
36	34.8	37.4	939	10	CG442723	CG442723 OCTAUI7TV
37	34.6	37.2	972	10	CM921961	CM921961 Telradon
38	34.6	37.2	1013	10	CM921961	CM921961 EDCAP72TR
39	34.4	37.0	501	2	BE360066	BE360066 DG1_61_G0
40	34.2	36.8	514	9	B2137695	B2137695 CH230-432
41	34.2	36.8	744	7	CK481107	CK481107 AGENCOURT
42	34	36.6	550	5	BO987803	BO987803 OGF13D16.
43	34	36.6	582	5	BU005353	BU005353 OGG7N20.Y
44	34	36.6	605	5	BQ861241	BQ861241 OGC17020.
45	34	36.6	650	5	BU08102	BU08102 OGH6104.Y

#### ALIGNMENTS

RESULT 1  
LOCUS A1909008 527 bp mRNA linear EST 30-MAR-2000  
DEFINITION QV-BT197-050499-038 BT197 Homo sapiens cDNA, mRNA sequence.  
VERSION A1909008.1 GI:6499688

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM

REFERENCE  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jorgensen,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL  
PUBMED Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil

Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/seq/gethtml.pl?cl=QV&cl=QV-BT197-038.html  
cl=050499&cl=1)  
Seq primer: puc 18 forward.

#### FEATURES

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/sex="female"  
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/note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2:





**Fri Nov 25 10:36:40 2005**

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DEFINITION	ZB96607.t1 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone IMAGE:330611.5 similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN) ; mRNA sequence.					
ACCESSION	W31998					
VERSION	W31998.1 GI:1313010					
KEYWORDS	EST					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryotic Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.					
AUTHORS	1 (bases 1 to 416) Hillier,L., Lennon,G., Becker,M., Bernaldo,M.F., Chiappelli,B., Chisnoe,S., Dietrich,N., Dubucq,T., Favello,A., Gish,N., Hawkins,E., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Marling,B., Moore,B., Morris,W., Parsons,J., Plange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thery-Weg,J., Treviskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.					
TITLE	Generation and analysis of 280,000 human expressed sequence tags					
JOURNAL	Genome Res. 6 (9), 807-828 (1996)					
PUBMED	8889549					
COMMENT	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estowatson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 771 Std Error: 0.00 Seq primer: mob.REGATET High quality sequence stop: 386. Location/Qualifiers 1..416 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:1258309" /db_xref="taxon:9606" /cds_start=IMAGE:320651 /clone="adult" /issue_type="parathyroid tumor" /dev_stage="adult" /lab_host="DHI08 (ampicillin resistant)" /clone_lib="Soares parathyroid tumor NBHPA" /note="Organ: parathyroid gland; Vector: pT73D (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-GGTTACCATCGTAGAGGAGCGGCAGCAAACTTTTTTTTTTTTTTTTTTTT TTTTT-3'] , double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT733 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Felina Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."					
ORIGIN						
Query Match	41.1%; Score 38.2; DB 8; Length 416;					
Best Local Similarity	64.7%; Pred. No. 0.63; 8; Indels 0; Gaps 0;					
Matches	33; Conservative 10; Mismatches					
Oy	42 UUCGACUCCUACUGAACGUUGAUUGCUUCGUAUUAAAACUCCAGACGCU 92      :     :     :     :     :     :     :     : Db      TCGAACTCGATGAGAGAGTGATGAGATGCTCGTAAGAACTCAGAGATT 124					
RESULT 7	W38764                    434 bp        mRNA        linear        EST 15-MAY-1996					
JOCUS	ZB27807.r1 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone					
DEFINITION	ZB27807.r1 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone					

ACCESSION	IMAGE:304788.5, similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
VERSION	M38764
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE	1 (bases 1 to 434) Hillier.L., Clark.N., Dubouque.T., Eliston.R., Hawkins.M., Holman.M., Holtzman.M., Kucab,T., Le.M., Lennon.G., Marra,M., Parsons.J.P., Rifkin,L., Rohlfing.T., Soares.M., Tan.F., Trevaeth.B., Waterson,R., Williams.A., Wohlmann,P. and Wilson.R. The M&N-Merck EST Project Unpublished (1995)
TITLE	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: mob.REGA+ET High quality sequence stop: 253. Location/Qualifiers
FEATURES	1..434 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:1248198" /db_xref="taxon:9606" /clone="IMAGE:304788" /tissue_type="parathyroid tumor" /dev_stage="adult" /lab_host="MDH0B (ampicillin resistant)." /clone_lib="Soares parathyroid tumor NBHPA" /note="Organ: parathyroid gland; Vector: PT73D [theta]"; with a modified polylinker; Site 1: Not I; Site 2:Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer 5'-GGTACCATCTCGAATGTGAAGCCGCCACCAATTTTTTCCTTTTTT TTT-3'); double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTZ193 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
ORIGIN	
Query Match	41.1%; Score 38.2; DB 8; Length 434;
Best Local Similarity	64.7%; Pred. No. 0.63;
Matches	33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
Dy	42 UCUGAACUCCAUAGAAAGUGUUAGAUCGCGCUAAAAAUCGACGAGCU 92    :   :   :   :   :   :   :   :   : 214 TCGGAACCTGATGAGAGTAGAAGTGCCTGAAGAAGCTGCAGAGATG 264
RESULT 8	
LOCUS	M56235
DEFINITION	ZC01E11.r1 Soares_parathyroid_tumor_NBHPA_homo_sapiens_cDNA clone IMAGE:321068.5, similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION	M56235
VERSION	M56235.1 GI:1358124
KEYWORDS	EST.



SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominae; Homo.  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Ellington, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
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/note="Organ: parathyroid gland; Vector: pRT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5'-TGTTACCAATCTGAAGTGGAGCGCGGACCAATTTTTTTTTTTTTTTT  
TTTTT-3'] double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."  
ORIGIN  
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Best Local Similarity 64.7%; Pred. No. 0.63;  
Matches 33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;  
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RESULT 9  
LOCUS W33077  
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ACCESSION W33077  
VERSION W33077.1  
KEYWORDS GI:1315062  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominae; Homo.

REFERENCE 1 (bases 1 to 453)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Ellington, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
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/note="Organ: parathyroid gland; Vector: pRT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5'-TGTTACCAATCTGAAGTGGAGCGCGGACCAATTTTTTTTTTTTTTTT  
TTTTT-3'] double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."  
ORIGIN  
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Best Local Similarity 64.7%; Pred. No. 0.63;  
Matches 33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;  
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Db 241 TCTGAATCGATGAGAGAGATGATGCGCTGTAAGAGCTGAGAGATGT 291  
RESULT 10  
LOCUS W56820  
DEFINITION zc01a03.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:321004 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.  
ACCESSION W56820  
VERSION W56820.1  
KEYWORDS GI:1358743  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominae; Homo.  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Ellington, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

FR1 NOV 25 10:36:40 2005

us-09-475-158a-16.rst

Page 6

TITLE  
JOURNAL  
COMMENT

Wrevasish, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.  
The Washu-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK

Email: [esowatson.watson@ecu.edu](mailto:esowatson.watson@ecu.edu)  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium ([info@image.lnlgov](mailto:info@image.lnlgov)) for further information.  
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clone="IMAGE:321004"
tissue_type="parathyroid tumor"
dev_stage="adult"
lab_host="DH10B (ampicillin resistant)"
clone_1ib="Soares parathyroid tumor NBHPA"
note="Organ: parathyroid gland; Vector: pT73d
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo (dT) primer
15'-GTTTACCATCTGTAGAGGAGGCGGCGACCAATTTTTTTTTTTTTTTTTT
TTTTT-3'", double-stranded cDNA was size selected, ligated
to Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT73d
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

```

ORIGIN			
Query Match	41.1%	Score 38.2;	DB 8; Length 496;
Best Local Similarity	64.7%	Pred. No. 0.64;	
Matches 33; Conservative	10;	Mismatches 8;	Indels 0; Gaps 0;

[illegible]

RESULT 11			
W52945	LOCUS	DEFINITION	
W52945	523 bp	mrna	linear
zc03h08.r1	Soares parathyroid tumor NBHPA Homo sapiens cDNA clone		EST 10-OCT-1996
IMAGE:212129.5	similar to gb:v00597	PARATHYROID HORMONE PRECURSOR (HUMAN) ;	mrna sequence.

ACCESSION	MS2945
VERSION	MS2945.1
KEYWORDS	GI:1350379
EST.	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 523)
AUTHORS	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

REFERENCE  
AUTHORS  
1 (bases 1 to 523)  
Hillier, L., Clark, N., Dubnue, T., Ellston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kuchba, T., Le, M., Lennon, G., Narra, M.,  
Parsons, J., Rifkin, L., Ruffing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
TITLE  
The Mashu-Merck EST Project  
JOURNAL  
Unpublished (1995)

COMMENT

COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel.: 314.286.1800  
Fax: 314.286.1810  
Email: [ees@wustl.edu](mailto:ees@wustl.edu)  
This clone is available royalty-free through LML; contact the  
IMAB Consortium ([info@image.lml.gov](mailto:info@image.lml.gov)) for further information.  
Insert Length: 702 Std Error: 0.00  
Seq primer: mob.RCGA+RT  
High quality sequence stop: 304.  
Location/Qualifiers  
1. 523

FEATURES

source

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FEATURES
Source
Location/Qualifiers
1..523
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/db_xref="taxon:9606"
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/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares.parathyroid.tumor_NBH9A"
/notes="Organ: parathyroid gland; Vector: pPT73D
(Pharmacia) with a modified polylinker; Site:1: Not I;
Site:2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer
5'..TGTTACCAATCTGAAGTCGAGCGCGCCACCAATTTTTTTTTTTTTTTTT
TTTTT-3'., double-stranded cDNA was size selected, ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT733
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

```

Query Match	41.1%	Score 38.2;	DB 8;	Length 523;
Best Local Similarity	64.7%;	Pred. NO. 0.65;		
Matches 33;	Conservative 10;	Mismatches 8;	Indels 0;	Gaps 0;

QY 42 UUCUAGACUCCACUAGACGUGUUGUAGUGGUCUGGUAUAAAAACUGCAGACGCU 92  
 Db 39 TCTGAACTCGATGCGAGAGTAGAATGCTGCTGTAAGCAGTCGACAGATGT 89

RESULT 12	LOCUS	DEFINITION
W19765	536 bp	RNA linear EST 03-MAY-1996
W19765	zb3sc03_r1 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone IMAGE:305966 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN) ;, mRNA sequence.	

ACCESSION W19765.1 GI:1295882  
 VERSION W19765.1 GI:1295882  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 536)  
 AUTHORS Hillier, L., Clark, N., Dubouque, T., Elliston, K., Hawkins, M.,

TITLE  
JOURNAL  
COMMENT

Treaskas, E., Waterston, R., Williamson, A., Wohlmann, P., Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800



```

/organism="Homo sapiens"
/mol_type="mRNA"
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/db_xref="taxon:9606"
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/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares parathyroid gland; vector: pT73D
(note: Organ: parathyroid gland; vector: pT73D
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer
5'-TGTACCAATCTGAAGTGGAGCGCGCCGACCAATTTTTTTTTTTTTTTT
TTTT-3'], double-stranded cDNA was size selected, ligated
to Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT73
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

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## ORIGIN

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Query Match      41.1%; Score 38.2; DB 8; Length 576;
Best Local Similarity 64.7%; Pred. No. 0.66;
Matches 33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

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Db      224 TCTGAACTCGATGAGAGAGTAGATGCTCGTAAAGACTGCAGATGT 274

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## RESULT 15

```

W39202      583 bp      mRNA      linear      EST 15-MAY-1996
LOCUS      235503.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
DEFINITION IMAGE:305621.5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
(HUMAN);, mRNA sequence.

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```

ACCESSION      W39202
VERSION      W39202.1
KEYWORDS      GI:1320911
SOURCE      EST.
ORGANISM      Homo sapiens (human)

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REFERENCE      Homo sapiens
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
      Homiidae; Homo.
      1 (bases 1 to 583)
      Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
      Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
      Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
      Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
      Wilson, R.

```

```

TITLE      The Washu-Merck EST Project
JOURNAL      Unpublished (1995)
COMMENT      Contact: Wilson RK
      Washington University School of Medicine
      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
      Tel: 314 286 1800
      Fax: 314 286 1810

```

## FEATURES

```

Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.RGA+ET
High quality sequence stop: 400.
Location/Qualifiers
1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1249031"
/db_xref="taxon:9606"
/clone_image="305621"

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/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares parathyroid tumor NbHPA"
(note: Organ: parathyroid gland; vector: pT73D
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer
5'-TGTACCAATCTGAAGTGGAGCGCGCCGACCAATTTTTTTTTTTTTTTT
TTTT-3'], double-stranded cDNA was size selected, ligated
to Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT73
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

```

## ORIGIN

```

Query Match      41.1%; Score 38.2; DB 8; Length 583;
Best Local Similarity 64.7%; Pred. No. 0.66;
Matches 33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

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```

QY      42 UCUGAACUCCAGGAGCGUGUGAUGGCGGCUAAAAACUGCAGGACGU 92
      :|:||||:|:||||:|:||||:|:||||:|:||||:|:||||:|:
Db      93 TCTGAACTCGATGAGAGAGTAGATGCTCGTAAAGACTGCAGATGT 143

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Search completed: November 24, 2005, 01:30:31
Job time : 1825 secs

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1	53.6	57.6	258	3	US-09-463-282D-26	Sequence 26, Appl
C 2	48.4	52.0	74	2	US-08-142-551B-132	Sequence 132, Appl
C 3	46.2	49.7	141	2	US-08-468-275-3	Sequence 3, Appl
C 4	46.2	49.7	141	2	US-08-468-275-5	Sequence 5, Appl
C 5	46.2	49.7	141	3	US-09-007-466-3	Sequence 3, Appl
C 6	46.2	49.7	141	3	US-09-007-466-5	Sequence 5, Appl
C 7	46.2	49.7	141	3	US-08-952-980B-3	Sequence 3, Appl
C 8	46.2	49.7	141	3	US-08-952-980B-5	Sequence 5, Appl
C 9	46.2	49.7	207	2	US-08-142-551B-8	Sequence 8, Appl
10	43.4	46.7	45	3	US-09-463-282D-5	Sequence 5, Appl
11	43	46.2	67	3	US-09-068-738A-9	Sequence 9, Appl
12	39.8	42.8	102	3	US-10-340-484-14	Sequence 14, Appl
13	39.8	42.8	234	2	US-08-733-446-19	Sequence 19, Appl
14	39.8	42.8	234	2	US-08-733-446-61	Sequence 61, Appl
15	39.8	42.8	217	2	US-08-733-446-20	Sequence 20, Appl
16	39.8	42.8	240	2	US-08-733-446-21	Sequence 21, Appl
17	39.8	42.8	243	2	US-08-733-446-22	Sequence 22, Appl
18	39.8	42.8	245	2	US-08-733-446-24	Sequence 24, Appl
C 19	39.8	42.8	247	2	US-08-733-446-25	Sequence 25, Appl
C 20	39.8	42.8	248	2	US-08-733-446-26	Sequence 26, Appl
C 21	39.8	42.8	250	2	US-08-733-446-27	Sequence 27, Appl
C 22	39.8	42.8	251	2	US-08-733-446-28	Sequence 28, Appl
C 23	39.8	42.8	252	2	US-08-689-190-1	Sequence 1, Appl
C 24	39.8	42.8	252	2	US-08-733-446-23	Sequence 23, Appl



Query Match 49.7%; Score 46.2; DB 3; Length 141;  
Best Local Similarity 51.6%; Pred. No. 4.8e-05;









Fri Nov 25 10:36:39 2005

RESULT 15  
US-08-733-446-20  
; Sequence 20, Application US/08733446  
; Patent No. 5856138  
; GENERAL INFORMATION:  
; APPLICANT: FUKUDA, Tsunehiko  
; TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTEINS AND  
; TITLE OF INVENTION: PRODUCTION THEREOF  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESSEE: CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/733,446  
; FILING DATE: 18-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/402,970  
; FILING DATE:  
; APPLICATION NUMBER: US/07/926,787  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: NEUNER, George W  
; REGISTRATION NUMBER: 26964  
; REFERENCE/DOCKET NUMBER: 42025  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)523-3400  
; TELEFAX: (617)523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 237 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid, synthetic DNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..237  
; IDENTIFICATION METHOD: E  
US-08-733-446-20

Query Match 42.8%; Score 39.8; DB 2; Length 237;  
Best Local Similarity 64.7%; Pred. No. 0.0049;  
Matches 33; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

Oy 42 UCUCGAACUCCGAUGGAACGUGUGAAUGGCGUGCGUAAAAACUGCAGGACGU 92  
Db 27 TTTCGAATCCATGGCGGTGATGAGATGGCTGGCTGAAGAGTTGCAGGATGT 77

Search completed: November 24, 2005, 01:34:15  
Job time : 74.6667 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 24, 2005, 01:30:39 ; Search time 195 Seconds  
(without alignments)

70.875 Million cell updates/sec

Title: US-09-475-158A-16

Perfect score: 93

Sequence: 1 gcguuuuccgaacggagg.....guaaaaacgcaggacguu 93

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3205263 seqs, 74304013 residues

Total number of hits satisfying chosen parameters: 6410526

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:

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- 2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq2.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq3.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	28.2	30.3	947	1	US-10-927-641-116
C 2	28.2	30.3	3507	1	US-10-509-422-1
C 3	28.2	30.3	3704	1	US-10-509-422-3
C 4	28	30.1	6497	1	US-10-821-234-839
C 5	26.4	28.4	3371	1	US-10-131-826A-35
C 6	25.2	27.1	2536	1	US-10-793-626-4301
C 7	25	26.9	1065	1	US-10-821-234-766
C 8	24.6	26.5	2218	1	US-10-821-234-119
C 9	24.4	26.2	2043	1	US-10-467-962B-100
C 10	24.4	26.2	3893	1	US-10-821-234-255
C 11	24.2	26.0	963	1	US-10-821-234-775
C 12	24	25.8	2748	1	US-10-526-731-4
C 13	23.8	25.6	1150	1	US-10-131-826A-531
C 14	23.8	25.6	5690	1	US-10-485-517-4
C 15	23.8	25.6	14770	1	US-10-821-234-268
C 16	23.4	25.2	477	1	US-10-467-962B-82
C 17	23.4	25.2	7008	1	US-10-821-234-758
C 18	23	24.7	445	1	US-10-802-796-374
C 19	23	24.7	1152	7	US-11-074-176-77
C 20	23	24.7	1849	7	US-11-015-546A-19
C 21	23	24.7	1956	1	US-10-994-820A-33
C 22	23	24.7	2292	7	US-11-013-247A-34
C 23	22.8	24.5	585	1	US-10-793-626-621

ALIGNMENTS

RESULT 1

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; Sequence 116, Application US/10927641  
; Publication No. US20050244968A1  
; GENERAL INFORMATION:  
; APPLICANT: Perera, Ranjan  
; APPLICANT: Rice, Stephen  
; APPLICANT: Eagleton, Claire  
; APPLICANT: Lasham, Annette  
; APPLICANT: Wood, Marion  
; APPLICANT: Visser, Elizabeth  
; TITLE OF INVENTION: Compositions and Methods for the  
; TITLE OF INVENTION: Modification of Gene Expression  
; FILE REFERENCE: 11000.1036c4  
; CURRENT APPLICATION NUMBER: US/10/927,641  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/137,036  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599  
; PRIOR FILING DATE: 1999-03-25  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 116  
; LENGTH: 947  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis  
US-10-927-641-116

Query Match 30.3%; Score 28.2; DB 1; Length 947;  
Best Local Similarity 56.1%; Pred. No. 1.7;  
Matches 23; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CUGUUCGAAUCCGUGUGUGUGUGUGUGUGUGUGUGU 42

Db 537 CAGTGCACCAATGCTGGTGGTGGTGGTGGTGGTGGT 497



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; ORGANISM: Homo sapiens
US-10-821-234-766

Query Match      26.9%; Score 25; DB 1; Length 1065;
Best Local Similarity 40.0%; Pred.No.16;
Matches 26; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

QY    4 GUUUCGAAAUCCGUUGCGUGGUGGUGGUGGUGGUGGUAACUCCAAGGAACGGUU 63
Db     264 GTTTCATGCCTGGTGCTGGGTGTGAGTGGCAGTCGTGGGCCGTGGTGGT 205

QY    64 GAAUG 68
Db     204 GCCTG 200

RESULT 8
US-10-821-234-119/c
; Sequence 119, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 119
; LENGTH: 2218
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-119

Query Match      26.5%; Score 24.6; DB 1; Length 2218;
Best Local Similarity 47.3%; Pred.No.25;
Matches 26; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY    16 GGUGUGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUAACUCCAAGGAACGGUUGAUGC 70
Db     1756 CGTGGTGGTGGTGGTGGTGGTTGAGACAGGCTCTGTCCCAGGCTGGAGTGC 1702

RESULT 9
US-10-467-962B-100/c
; Sequence 100, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Biau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000 857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 100
; LENGTH: 2043
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2043)
; OTHER INFORMATION: ORF K5J14.11, Linie 229091
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US-10-467-962B-100

Query Match 26.2%; Score 24.4; DB 1; Length 2043;  
Best Local Similarity 69.2%; Pred. No. 29;  
Matches 18; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 12 AAUCCGUGGUGGUGGUGGUGGUGG 37  
Db 89 AAGCGGTGGTGGTGGTGGTGGTGGT 64

RESULT 10

US-10-821-234-255/c  
; Sequence 255, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 255  
; LENGTH: 3893  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-821-234-255

Query Match 26.2%; Score 24.4; DB 1; Length 3893;  
Best Local Similarity 61.5%; Pred. No. 32;  
Matches 16; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 17 GUGGUGGUGGUGGUGGUGGUGGU 42  
Db 2641 GTGGTGGTGGTGGTGGTGGTGGT 2616

RESULT 11

US-10-821-234-775  
; Sequence 775, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 775  
; LENGTH: 963  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-821-234-775

Query Match 26.0%; Score 24.2; DB 1; Length 963;  
Best Local Similarity 51.4%; Pred. No. 29;  
Matches 19; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 3 UGUUUCGAUACGUGGUGGUGGUGGUGGU 39  
Db 591 TGGTTCGGAACTTGTGGTGGTGGTGGT 627

RESULT 12

US-10-526-731-4  
; Sequence 4, Application US/10526731  
; Publication No. US20050244437A1  
; GENERAL INFORMATION:  
; APPLICANT: AKZO Nobel N.V.  
; TITLE OF INVENTION: live attenuated parasite vaccine  
; FILE REFERENCE: 2002-017-BF  
; CURRENT APPLICATION NUMBER: US/10/526,731  
; CURRENT FILING DATE: 2005-03-04  
; PRIOR APPLICATION NUMBER: EP 02078953  
; PRIOR FILING DATE: 2002-09-20  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 2748  
; TYPE: DNA  
; ORGANISM: Toxoplasma gondii  
US-10-526-731-4

Query Match 25.8%; Score 24; DB 1; Length 2748;  
Best Local Similarity 54.2%; Pred. No. 40;  
Matches 26; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 38 GUGUCUGAACUCCAGGACGUGUGAUGGCGGUAAAAACUCC 85  
Db 2021 GTGCTGTGCGCCATGCGACAGCAGATCGTTCGTACAAAGCTTC 2068

RESULT 13

US-10-131-826A-531  
; Sequence 531, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerriksen, Wary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C128  
; CURRENT APPLICATION NUMBER: US/10/131,826A  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 16:17:24 ; Search time 186 Seconds

(without alignments)  
37.796 Million cell updates/sec

Title: SEQ-NEW

Perfect score: 83

Sequence: 1 avseiqmhnlgsggg 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq\_21.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	85.5	450	3	AAY96988 Human tet
2	69	83.1	31	3	AAY96975 Parathyro
3	62	74.7	31	3	AAY96973 Parathyro
4	62	74.7	38	2	AAR58104 [Gly13]-h
5	59	71.1	12	9	ADZ76826 Parathyro
6	59	71.1	13	6	ABG76365 Mutant pe
7	59	71.1	14	3	ABO1861 [Ala1]-pa
8	59	71.1	14	4	AAB96896 Rat parat
9	59	71.1	14	4	AAB84776 Native ra
10	59	71.1	14	8	ADU24382 Novel hum
11	59	71.1	14	8	ADU24382 Novel hum
12	59	71.1	14	9	ADM88336 Rat parat
13	59	71.1	15	9	ADZ76832 Parathyro
14	59	71.1	21	6	ADP71487 Rat parat
15	59	71.1	21	9	ADM88343 Rat parat
16	59	71.1	27	3	AAY98016 Human ami
17	59	71.1	27	3	AAY98049 Human par
18	59	71.1	27	3	AAY98045 Human par
19	59	71.1	28	3	AAY98048 Human par
20	59	71.1	28	3	AAY98044 Human par
21	59	71.1	30	5	AAU73060 Parathyro
22	59	71.1	30	8	ADQ75375 PTH/PTHrP
23	59	71.1	31	2	AAY04203 Human par
24	59	71.1	31	3	AAY96978 PTH-rp fu

25	59	71.1	31	7	ADI24779	Parathyro
26	59	71.1	33	3	AAY98015	Human ami
27	59	71.1	34	1	AAP82177	Sequence
28	59	71.1	34	1	AAR07920	Rat parat
29	59	71.1	34	2	AAR07917	Rat parat
30	59	71.1	34	2	AAR62432	Accelerat
31	59	71.1	34	2	AAR99980	Rat parat
32	59	71.1	34	2	AAW19996	Cyclised
33	59	71.1	34	2	AAW20002	Cyclised
34	59	71.1	34	2	AAW20008	Cyclised
35	59	71.1	34	2	AAY98014	Human ami
36	59	71.1	34	3	AAB91100	Parathyro
37	59	71.1	34	4	AAB96897	Rat parat
38	59	71.1	34	4	AAB84777	Native hu
39	59	71.1	34	5	AAU73037	Parathyro
40	59	71.1	34	6	ABP71499	Rat parat
41	59	71.1	34	6	AAO27426	Mouse mat
42	59	71.1	34	6	AAO27425	Rat matur
43	59	71.1	34	8	ADP04395	Norway ra
44	59	71.1	34	8	ADQ75352	PTH/PTHrP
45	59	71.1	34	8	ADR14832	Amino aci
46	59	71.1	34	8	ADT94476	Exemplary
47	59	71.1	34	8	ADT94475	Rat PTH (
48	59	71.1	34	9	ADX15519	Parathyro
49	59	71.1	35	2	AAR74466	Parathyro
50	59	71.1	36	2	AAR58248	N-Dimethy
51	59	71.1	36	2	AAR58026	N-alpha-m
52	59	71.1	36	2	AAR58262	[Ala1]-hp
53	59	71.1	37	4	AAB86231	Rat parat
54	59	71.1	38	2	AAR58019	N-alpha-m
55	59	71.1	84	5	AAE23747	Rat PTH p
56	59	71.1	84	5	AAU73023	Parathyro
57	59	71.1	84	5	ABG72602	Rat bioac
58	59	71.1	84	6	ABG72603	Mouse bio
59	59	71.1	84	7	ADA39531	Rat parat
60	59	71.1	84	8	ADF77381	Parathyro
61	59	71.1	84	8	ADQ75338	PTH/PTHrP
62	59	71.1	84	8	ADT98117	Mouse par
63	59	71.1	84	8	ADT98117	Rat parat
64	59	71.1	84	9	ADX15518	Rat PTH (
65	59	71.1	84	9	ADX15531	Rat PTH (
66	59	71.1	84	9	ADZ76842	Rat parat
67	59	71.1	84	9	ADZ76843	Mouse par
68	59	71.1	84	9	ADZ76835	Rat parat
69	59	71.1	84	9	ADZ76836	Mouse par
70	59	71.1	115	1	AAP80308	Sequence
71	59	71.1	115	7	ADD47895	Rat Prote
72	59	71.1	115	8	ADJ36448	Mus muscu
73	59	71.1	115	8	ADJ36460	Mus muscu
74	59	71.1	115	8	ADJ36472	Rat parat
75	59	71.1	115	8	ADJ36455	Rat parat
76	59	71.1	115	8	ADJ36470	Rat parat
77	58	69.9	38	2	AAR58024	[Ala1,1le
78	57	68.7	31	7	ADI24780	Human par
79	57	68.7	31	7	ADI24780	Parathyro
80	57	68.7	35	2	AAR74470	Parathyro
81	56	67.5	12	2	AAW99450	Human par
82	56	67.5	13	2	AAW99450	Mutant pe
83	56	67.5	13	6	ABG76366	Human par
84	56	67.5	14	3	AAB01859	Human par
85	56	67.5	14	4	AAB96894	Human par
86	56	67.5	14	4	AAB84773	Native hu
87	56	67.5	14	8	ADR14863	Amino aci
88	56	67.5	14	8	ADU24391	Human par
89	56	67.5	15	9	ADZ76830	Parathyro
90	56	67.5	17	2	AAR94192	Human par
91	56	67.5	21	6	ABP71486	Human par
92	56	67.5	21	9	ADM88342	Human par
93	56	67.5	27	3	AAY98019	Human ami
94	56	67.5	27	3	AAY98047	Human par
95	56	67.5	27	3	AAY98053	Human par
96	56	67.5	28	2	AAR88838	Human par
97	56	67.5	28	2	AAR88837	Human par



CC and disorders associated with decreased tether1 activity, increasing CAMP  
 CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
 CC non-peptide PTH (claimed). The new compound can be administered by  
 CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
 CC regular injections to treat osteoporosis  
 XX  
 SQ Sequence 31 AA;  
 Query Match 83.1%; Score 69; DB 3; Length 31;  
 Best Local Similarity 87.5%; Pred. No. 0.00085;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 AVSEIQLMHLNGLGGGG 16  
 Db 1 AVSEIQLMHLNGLGGGG 16  
 RESULT 3  
 ID AAY96973 standard; peptide; 31 AA.  
 XX  
 AC AAY96973;  
 DT 31-OCT-2000 (first entry)  
 XX  
 DE Parathyroid hormone functional domain conjugate peptide PG5.  
 XX  
 KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;  
 KW resorption; remodeling; tether1; osteoporosis.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 Key Location/Qualifiers  
 FH 1..9  
 FT Peptide /label= PTH N-terminal\_signaling\_domain  
 FT /note= "residues 1-9"  
 FT Peptide 10..14  
 FT /label= linker  
 FT Peptide 15..30  
 FT /label= PTH C-terminal\_binding\_portion  
 FT /note= "residues 15-31"  
 XX  
 PN WO200039278-A2.  
 XX  
 XX 06-JUL-2000.  
 XX  
 XX 30-DEC-1999; 99WO-US031108.  
 XX  
 XX 31-DEC-1998; 98US-0114577P.  
 XX  
 XX (GARD/) GARDELLA T J.  
 XX (KRON/) KRONENBERG H M.  
 XX (POTT/) POTTS J T.  
 XX (JUEP/) JUEPPNER H.  
 XX  
 XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 XX  
 XX WPI; 2000-452384/39.  
 XX N-PSDB; AAA51729.  
 XX  
 XX New compound comprising an amino terminal signaling functional domain  
 XX linked to a carboxy-terminal binding portion of parathyroid hormone for  
 XX treating mammalian conditions characterized by decreases in bone mass.  
 XX  
 XX Claim 7; Page 92-93; 119pp; English.  
 XX  
 XX Compounds of the structure or formula S-(L)<sub>n</sub>-B, R<sub>1</sub>-S-(L)<sub>n</sub>-R or S-(L)<sub>n</sub>-  
 XX -R, are new. S is an amino terminal signaling functional domain of  
 XX parathyroid hormone (PTH); L is a linker molecule present n times (where  
 XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
 XX portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R<sub>1</sub> is the  
 XX PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor

CC sequence. The new compounds are used for treating mammalian conditions  
 CC characterized by decreases in bone mass, determining rates of bone  
 CC reformation, bone resorption and/or bone remodeling, treating diseases  
 CC and disorders associated with decreased tether1 activity, increasing CAMP  
 CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
 CC non-peptide PTH (claimed). The new compound can be administered by  
 CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
 CC regular injections to treat osteoporosis  
 XX  
 SQ Sequence 31 AA;  
 Query Match 74.7%; Score 62; DB 3; Length 31;  
 Best Local Similarity 87.5%; Pred. No. 0.011;  
 Matches 14; Conservative 0; Mismatches 0; Indels 2; Gaps 1;  
 Qy 1 AVSEIQLMHLNGLGGGG 16  
 Db 1 AVSEIQLMHLNGLGGGG 14  
 RESULT 4  
 ID AAR58104 standard; peptide; 38 AA.  
 XX  
 AC AAR58104;  
 XX  
 DT 20-SEP-1994 (first entry)  
 XX  
 DE [Gly13]-hPTH(1-38)-OH.  
 XX  
 KW Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;  
 KW fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.  
 XX  
 OS Synthetic.  
 XX  
 PN GB2269176-A.  
 XX  
 PD 02-FEB-1994.  
 XX  
 PF 12-JUL-1993; 93GB-00014384.  
 XX  
 PR 15-JUL-1992; 92GB-00015009.  
 PR 18-DEC-1992; 92GB-00026415.  
 PR 23-DEC-1992; 92GB-00026859.  
 PR 23-DEC-1992; 92GB-00026861.  
 PR 28-JAN-1993; 93GB-00001691.  
 PR 28-JAN-1993; 93GB-00001692.  
 PR 14-APR-1993; 93GB-00007673.  
 PR 19-APR-1993; 93GB-00008033.  
 XX  
 XX (SANO ) SANDOZ LTD.  
 XX  
 XX Lewis I, Schneider H, Waelchli R, Rainer A;  
 XX WPI; 1994-018352/03.  
 XX  
 XX New active para-thyroid hormone variants - used for treating or  
 XX preventing osteoporosis etc.  
 XX  
 XX Example 101; Page 39; 92pp; English.  
 XX  
 XX This peptide is an example of a highly generic formula covering  
 XX parathyroid hormone variants useful for treating or preventing bone  
 XX conditions associated with calcium depletion/resorption, in cases where  
 XX calcium fixation is required (esp. osteoporosis) or to treat  
 XX hypoparathyroidism  
 XX  
 SQ Sequence 38 AA;  
 Query Match 74.7%; Score 62; DB 2; Length 38;  
 Best Local Similarity 92.3%; Pred. No. 0.014;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 13  
 Db :|||||  
 1 SVSEIQLMHNLG 13

RESULT 5  
 ADZ76826  
 ID ADZ76826 standard; peptide; 12 AA.  
 XX  
 AC ADZ76826;  
 XX  
 DT 14-JUL-2005 (first entry)  
 XX  
 DE Parathyroid hormone (PTH) (1-12) antigenic peptide, SEQ ID NO: 5.  
 XX  
 DE Parathormone; PTH; hormone; antigen.  
 KW  
 XX Mus musculus.  
 OS Rattus sp.  
 XX  
 PN US2005095236-A1.  
 XX  
 PD 05-MAY-2005.  
 XX  
 PF 29-NOV-2004; 2004US-00998927.  
 XX  
 PR 05-DEC-2000; 2000US-00730174.  
 XX  
 PA (ZHR/) ZAHRADNIK R J.  
 PA (LAVI/) LAVIGNE J R.  
 XX  
 PI Zahradnik RJ, Lavigne JR;  
 DR WPI, 2005-344980/35.  
 XX  
 PT Producing antibodies to the N-terminal portion of (1-84) parathyroid  
 PT hormone (PTH) by administering a first peptide antigen to a host animal,  
 PT useful in determining bioactive intact PTH levels in serum, plasma and/or  
 PT cell culture media.  
 XX  
 PS Claim 1; SEQ ID NO 5; 13pp; English.

XX The present invention relates to a method of producing an antibody to the  
 CC N-terminal portion of (1-84) parathyroid hormone (PTH) which comprises  
 CC administering N-terminal peptide antigens corresponding to amino acid  
 CC residues 2-12, 1-12, 2-15 and 1-15 of PTH. The methods and compositions  
 CC of the invention are useful in determining bioactive intact PTH levels in  
 CC serum, plasma and/or cell culture media and antibodies possessing a high  
 CC degree of species cross-reactivity. The present sequence is a parathyroid  
 CC hormone (PTH) (1-12) antigenic N-terminal peptide. This N-terminal  
 CC peptide sequence is obtained from mouse and rat species.

XX Sequence 12 AA;  
 SQ

Query Match 71.1%; Score 59; DB 9; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 12  
 Db :|||||  
 1 AVSEIQLMHNLG 12

RESULT 6  
 ABG76365  
 ID ABG76365 standard; peptide; 13 AA.  
 XX  
 AC ABG76365;  
 XX  
 DT 19-MAY-2003 (first entry)  
 XX  
 DE Mutant peptide #2 derived from human parathyroid hormone (hPTH).  
 XX  
 PF

KW Human; three-dimensional epitope; human parathyroid hormone; hPTH;  
 KW bioactive hPTH; antibody production; hyperparathyroidism; antithyroid;  
 KW hypoparathyroidism; immunostimulant; mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO2003003986-A2.  
 XX  
 PD 16-JAN-2003.  
 XX  
 PF 03-JUL-2002; 2002WO-US021356.  
 XX  
 PR 03-JUL-2001; 2001US-00898398.  
 XX  
 PA (QUES-) QUEST DIAGNOSTICS INVESTMENTS INC.  
 XX  
 PI Hutchison JS;  
 XX  
 DR WPI, 2003-229379/22.  
 XX  
 PT Producing antibodies to a three-dimensional epitope of a bioactive human  
 PT parathyroid hormone for diagnosing or treating e.g., hyperparathyroidism  
 PT by immunizing an animal with the hormone and recovering the antibodies.  
 XX  
 PF Disclosure; Page 10; 69pp; English.

XX The present invention relates to a method for producing antibodies to a  
 CC three-dimensional epitope of bioactive human parathyroid hormone (hPTH).  
 CC The method comprises immunising an animal with the bioactive hPTH and  
 CC recovering antibodies from the animal. The antibodies specifically  
 CC recognise the three-dimensional structure of the bioactive hPTH. The  
 CC method is useful for manufacturing a medicament for diagnosing or  
 CC treating hyperparathyroidism or hypoparathyroidism. ABG76364-ABG76370  
 CC represent mutants or "variants" of peptide sequences from hPTH

XX Sequence 13 AA;  
 SQ

Query Match 71.1%; Score 59; DB 6; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 12  
 Db :|||||  
 1 AVSEIQLMHNLG 12

RESULT 7  
 AAB01861  
 ID AAB01861 standard; peptide; 14 AA.  
 XX  
 AC AAB01861;  
 XX  
 DT 11-SEP-2000 (first entry)  
 XX  
 DE [Ala1]-parathyroid hormone peptide(1-14), SEQ ID NO:5.  
 XX  
 KW Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;  
 KW calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;  
 KW bone synthesis; agonist; osteoporosis; non-parenteral delivery.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT Modified-site 14  
 FT /note= "C-terminal amide"  
 XX  
 PN WO200023594-A1.  
 XX  
 PD 27-APR-2000.  
 XX  
 PF 20-OCT-1999; 99WO-US024481.

XX 22-OCT-1998; 98US-0105530P.  
 PR (GARD/) GARDELLA T J.  
 XX (KRON/) KRONENBERG H M.  
 PA (POTT/) POTTS J T.  
 PA (JUEP/) JUEPPNER H.  
 XX  
 XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 XX WPI; 2000-339693/29.  
 XX  
 XX Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic  
 XX acids that encode them, useful for treating osteoporosis.  
 PT  
 XX Claim 3; Page 47; 73pp; English.  
 PS  
 XX The invention relates to a novel parathyroid hormone (PTH) peptide  
 CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and  
 CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-  
 CC B01863). The peptides of the invention are at least 85% identical to the  
 CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-  
 CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is  
 CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;  
 CC provided that the peptide is not PTHrP(1-14). The peptides of the  
 CC invention also encompass fragments of peptides of the invention  
 CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-  
 CC terminal derivatives. PTH is a major regulator of calcium homeostasis,  
 CC and is necessary for the normal function of the gastrointestinal,  
 CC skeletal, neurological system, neuromuscular and cardiovascular systems.  
 CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,  
 CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic  
 CC effect on the skeleton, and mediates calcium reabsorption, enhances  
 CC phosphate clearance and vitamin D synthesis in the kidney. A homologous  
 CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of  
 CC the renal and skeletal actions of PTH, and also bind to the PTH-1  
 CC receptor. They do not bind to the PTH-2 receptor. The peptides of the  
 CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,  
 CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-  
 CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of  
 CC conditions characterised by a decrease in bone mass, such as  
 CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating  
 CC medical disorders that arise from excessive or altered action of the PTH-  
 CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also  
 CC useful in the determination of rates of bone formation, bone resorption  
 CC and/or bone remodelling in a patient. The peptides of the invention are  
 CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by  
 CC conventional synthetic chemistry, and can be delivered to a patient via  
 CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent  
 CC PTH-1/PTH-2 receptor agonists  
 XX  
 XX Sequence 14 AA;  
 SQ  
 Query Match 71.1%; Score 59; DB 3; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AVSEIQLMHNLG 12  
 Db 1 AVSEIQLMHNLG 12  
 RESULT 8  
 AAB96896  
 ID AAB96896 standard; peptide; 14 AA.  
 AC AAB96896;  
 XX  
 XX 13-JUL-2001 (first entry)  
 DT  
 DE Rat parathyroid hormone (1-14).  
 XX Rat; human; parathyroid hormone derivative; calcium homeostasis;  
 KW  
 hypercalcaemia; anaemia; bone disease; renal impairment; ulcer; myopathy;  
 neuropathy; hyperparathyroidism; osteoporosis; fracture;  
 cartilage disorder.  
 KW Rattus sp.  
 XX WO200123427-A1.  
 XX 05-APR-2001.  
 PD 25-FEB-2000; 2000WO-US004716.  
 XX 29-SEP-1999; 99US-0156927P.  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 PI WPI; 2001-343161/36.  
 XX Novel amino acid encoding polypeptides useful in the treatment of  
 DR osteoporosis.  
 PT Example 2; Page 64; 100pp; English.  
 XX The present invention provides a number of parathyroid hormone  
 CC derivatives based on the rat and human hormone sequences. These peptides  
 CC can be used in the treatment of human skeletal conditions, including  
 CC osteoporosis, fractures and cartilage disorders, disruption of calcium  
 CC homeostasis, which may cause severe bone disease, anaemia, renal  
 CC impairment, ulcers, myopathy and neuropathy, hypercalcaemia and  
 CC hyperparathyroidism. The present peptide was used in the exemplification  
 CC of the invention  
 XX Sequence 14 AA;  
 SQ  
 Query Match 71.1%; Score 59; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AVSEIQLMHNLG 12  
 Db 1 AVSEIQLMHNLG 12  
 RESULT 9  
 AAB84776  
 ID AAB84776 standard; peptide; 14 AA.  
 XX AAB84776;  
 AC  
 XX 25-JUL-2001 (first entry)  
 DT  
 XX Native rat parathyroid hormone peptide fragment #1.  
 DE  
 XX Osteopathic; calcium homeostasis regulator; parathyroid hormone; PTH;  
 XX bone mass; osteoporosis.  
 KW  
 XX Rattus sp.  
 OS  
 XX WO200123521-A2.  
 XX 05-APR-2001.  
 PD 29-SEP-2000; 2000WO-US026818.  
 XX 25-SEP-1999; 99US-0156927P.  
 XX 25-FEB-2000; 2000US-0185060P.  
 PR  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 PI WPI; 2001-343161/36.  
 XX Novel amino acid encoding polypeptides useful in the treatment of  
 DR osteoporosis.  
 PT Example 2; Page 64; 100pp; English.  
 XX The present invention provides a number of parathyroid hormone  
 CC derivatives based on the rat and human hormone sequences. These peptides  
 CC can be used in the treatment of human skeletal conditions, including  
 CC osteoporosis, fractures and cartilage disorders, disruption of calcium  
 CC homeostasis, which may cause severe bone disease, anaemia, renal  
 CC impairment, ulcers, myopathy and neuropathy, hypercalcaemia and  
 CC hyperparathyroidism. The present peptide was used in the exemplification  
 CC of the invention  
 XX Sequence 14 AA;  
 SQ

XX	The specification describes a method for treating mammalian conditions
CC	characterized by a decrease in bone mass. The method comprises
CC	administering to a subject a biologically active peptide of a formula
CC	given in the specification. The peptide is a parathyroid hormone (PTH)
CC	derivative containing amino acid substitutions at selected positions in
CC	the polypeptide as well as derivatives containing lactam bridges between
CC	residues 6 and 10. The derivatives function as agonists of the PTH-1
CC	receptor. The method is useful in treating mammalian conditions
CC	characterized by a decrease in bone mass e.g. old age or post-menopausal
CC	osteoporosis. The present sequence represents a native rat PTH fragment.
XX	Sequence 14 AA;
SQ	
	Query Match                 71.1%; Score 59; DB 8; Length 14;
	Best Local Similarity      100.0%; Pred. No. 0.014;
	Matches          12; Conservative          0; Mismatches          0; Indels          0; Gaps          0
OY	1 AVSEIQLMHNLG 12
Db	1 AVSEIQLMHNLG 12
RESULT 11	
ID ADU24382	
ID ADU24382 standard; peptide; 14 AA.	
AC ADU24382;	
DT 27-JAN-2005 (first entry)	
DE Novel human parathyroid hormone-derived active peptide SeqID17.	
KW biologically active peptide; parathyroid hormone analogue; endocrine-Gen;	
KW antihypoid; cardiovascular-Gen; CNS-Gen; gastrointestinal-Gen;	
KW osteopathic; CAMP agonist; bone calcification promoter;	
KW parathyroid hormone-1 receptor agonist; calcium antagonist; bone mass;	
KW bone reformation; bone resorption; bone remodeling; osteoporosis;	
KW osteopenia; bone fracture; cartilage disorder; OTH-1 receptor; human.	
XX Homo sapiens.	
OS Synthetic.	
XX Key Location/Qualifiers	
FT Modified-site 14	
FT /note= "C-terminal amide"	
PN WO2004093902-A1.	
PD 04-NOV-2004.	
PF 19-MAR-2003; 2003WO-US008261.	
PR 19-MAR-2003; 2003WO-US008261.	
XX (GHEO ) GEN HOSPITAL CORP.	
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.	
PI Gardella TJ, Potte JT, Kronenberg HM, Shimizu N, Carter P;	
DR WPI ; 2004-795421/78.	
PT New conformationally constrained parathyroid hormone analogs and	
PT derivatives of those homologs, useful for raising cAMP levels in cells	
PT and treating conditions such as hyperparathyroidism and hypocalcemia.	
PS Disclosure; SEQ ID NO 17; 88pp; English.	
XX This invention relates to a novel biologically active peptide	
CC (conformationally constrained parathyroid hormone analogues and	
CC derivatives of those homologues). The invention may be useful for the	
CC development of compounds with an endocrine-Gen, antihypoid,	
CC cardiovascular-Gen, CNS-Gen, gastrointestinal-Gen or osteopathic activity	

CC acting as a CAMP agonist, bone calcification promoter, agonist of  
 CC parathyroid hormone-1 receptor or calcium antagonist. The invention may  
 CC be useful for treating mammalian conditions associated with decrease in  
 CC bone mass or for determining rates of bone reformation, bone resorption  
 CC and/or bone remodeling. The invention may also be useful for prophylaxis  
 CC and/or treatment of disorders associated with undesired bone loss, for  
 CC example osteoporosis, osteopenia, fractures and cartilage disorders, and  
 CC for treating a medical disorder that results from altered or excessive  
 CC action of the OTH-1 receptor. The present sequence is that of a human  
 CC parathyroid hormone-derived biologically active peptide of the invention.  
 XX  
 SQ Sequence 14 AA;

Query Match 71.1%; Score 59; DB 8; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 12  
 DB 1 AVSEIQLMHNLG 12  
 |||||

RESULT 12  
 ADW88336  
 ID ADW88336 standard; peptide; 14 AA.

AC ADW88336;

DT 21-APR-2005 (first entry)

DE Rat parathyroid hormone.

KW Cardiovascular-gen.; CNS-gen.; gastrointestinal-gen.; endocrine-gen.;  
 KW antihypertoid; parathormone; hypercalcemia; metabolic disorder.

OS Rattus sp.

FH Key Location/Qualifiers  
 FT Modified-site 14  
 FT /note= "C-terminal amide"

XX WO2005009358-A2.

XX 03-FEB-2005.

XX 16-JUL-2004; 2004WO-US022830.

XX 17-JUL-2003; 2003US-0487589P.

XX (GEHO ) GEN HOSPITAL CORP.

XX Gardella TJ;

XX WPI; 2005-132386/14.

XX New conformationally constrained parathyroid hormone analogs useful in  
 PT the treatment of e.g. hypercalcemia primary and hyperparathyroidism.

XX Disclosure; SEQ ID NO 26; 49pp; English.

XX The invention provides novel antagonists of the juxtaposition (J) domain  
 CC of the parathyroid hormone (PTH or parathormone) receptor. These  
 CC antagonists contain amino acid substitutions at selected positions in  
 CC truncated PTH and PTH-related polypeptide and function by selectively  
 CC binding the J domain of the receptor. The J domain is the region of the  
 CC receptor (PIR) that spans the seven transmembrane domain and the  
 CC extracellular loops. PIR polypeptide antagonists of the invention can be  
 CC used to treat conditions relating to PH/PIR hyperactivity, such as  
 CC hypercalcemia including malignant hypercalcemia (claimed), primary  
 CC hyperparathyroidism, and Jansen's chondrodysplasia. They can also be used  
 CC to identify other ligands (e.g. using a high-throughput screen) that bind  
 CC to PIR, such as small molecule PTH mimetic compounds, or for the  
 CC pharmacological analysis of PIR ligands for their selectivity, e.g. for

CC the J domain. The present sequence is that of rat PTH(1-14). PTH  
 CC derivatives of the invention contain changes in sequence relative to this  
 CC wild-type sequence. Note: this sequence is given as SEQ ID NO:26 in  
 CC Figure 1 of the specification, but is different from the sequence given  
 CC in SEQ ID NO:26 on page 16 ADW88342.

XX Sequence 14 AA;

Query Match 71.1%; Score 59; DB 9; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 12  
 DB 1 AVSEIQLMHNLG 12  
 |||||

RESULT 13  
 ADZ76832  
 ID ADZ76832 standard; peptide; 15 AA.

XX ADZ76832;

DT 14-JUL-2005 (first entry)

DE Parathyroid hormone (PTH) (1-15) antigenic peptide, SEQ ID NO: 11.

XX Parathormone; PTH; hormone; antigen.

XX Mus musculus.

XX Rattus sp.

XX US2005095236-A1.

XX 05-MAY-2005.

XX 29-NOV-2004; 2004US-00989827.

XX 05-DEC-2000; 2000US-00730174.

XX (ZAHN/) ZAHRADNIK R J.  
 XX (LAVI/) LAVIGNE J R.

XX Zahradnik RJ, Lavigne JR;

XX WPI; 2005-344980/35.

XX Producing antibodies to the N-terminal portion of (1-84) parathyroid  
 PT hormone (PTH) by administering a first peptide antigen to a host animal,  
 PT useful in determining bioactive intact PTH levels in serum, plasma and/or  
 PT cell culture media.

XX Disclosure; SEQ ID NO 11; 13pp; English.

XX The present invention relates to a method of producing an antibody to the  
 CC N-terminal portion of (1-84) parathyroid hormone (PTH) which comprises  
 CC administering N-terminal peptide antigens corresponding to amino acid  
 CC residues 2-12, 1-12, 2-15 and 1-15 of PTH. The methods and compositions  
 CC of the invention are useful in determining bioactive intact PTH levels in  
 CC serum, plasma and/or cell culture media and antibodies possessing a high  
 CC degree of species cross-reactivity. The present sequence is a parathyroid  
 CC hormone (PTH) (1-15) antigenic N-terminal peptide. This N-terminal  
 CC peptide sequence is obtained from mouse and rat species.

XX Sequence 15 AA;

Query Match 71.1%; Score 59; DB 9; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.015;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 12  
 DB 1 AVSEIQLMHNLG 12  
 |||||

RESULT 14  
 ABP71487  
 ID ABP71487 standard; peptide; 21 AA.  
 XX  
 AC ABP71487;  
 XX  
 DT 15-MAY-2003 (first entry)  
 XX  
 DE Rat parathyroid hormone (PTH) peptide fragment (residues 1-21).  
 XX  
 KW PTH; parathyroid hormone, anabolic; cAMP; bone mass; osteopenia; rat.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO2003009804-A2.  
 XX  
 PD 06-FEB-2003.  
 XX  
 PF 19-JUL-2002; 2002WO-US022922.  
 XX  
 PR 23-JUL-2001; 2001US-0306866P.  
 XX  
 PR 02-OCT-2001; 2001US-0326212P.  
 XX  
 PA (GARD/) GARDELLA T J.  
 XX  
 PI Gardella TJ;  
 XX  
 DR WPI; 2003-268010/26.  
 XX  
 PT Conformationally constrained parathyroid hormone (PTH) analogs, useful  
 PT for treating conditions characterized by decrease in bone mass (e.g.  
 PT osteoporosis) or by the need for bone growth (e.g. in treating fractures  
 PT or cartilage disorders).  
 XX  
 PS Disclosure; Page 114; 135pp; English.  
 XX  
 The invention relates to conformationally constrained parathyroid hormone  
 (PTH) analogues, in particular, derivatives of PTH (1-34), PTH (1-21),  
 PTH (1-20), PTH (1-19), PTH (1-318), PTH (1-17), PTH (1-16), PTH (1-15),  
 PTH (1-14), PTH (1-13), PTH (1-12), PTH (1-11), and PTH (1-10)  
 polypeptides. The PTH peptide analogues are useful for treating mammalian  
 conditions characterized by decrease in bone mass (e.g. old age  
 osteoporosis, post-menopausal osteoporosis) or by the need for bone  
 growth for e.g. in treating fractures or cartilage disorders and for  
 raising cyclic adenosine monophosphate (cAMP) levels in cells. They are  
 also useful for treating osteopenia. The PTH peptide analogues can also  
 be used as diagnostic probes, as antigens to prepare antibodies for use  
 as diagnostic probes and as molecular weight markers. The present  
 sequence represents a rat native PTH peptide fragment  
 XX  
 Sequence 21 AA;  
 Query Match 71.1%; Score 59; DB 6; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.022;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AVSEIQLMHNLG 12  
 DB 1 AVSEIQLMHNLG 12  
 RESULT 15  
 ADW88343  
 ID ADW88343 standard; peptide; 21 AA.  
 XX  
 AC ADW88343;  
 XX  
 DT 21-APR-2005 (first entry)  
 XX  
 DE Rat parathyroid hormone.  
 XX

KW Cardiovascular-gen.; CNS-gen.; gastrointestinal-gen.; endocrine-gen.;  
 KW antihypertoid; parathormone; hypercalcemia; metabolic disorder.  
 OS Rattus sp.  
 XX  
 PN WO2005009358-A2.  
 XX  
 PD 03-FEB-2005.  
 XX  
 PF 16-JUL-2004; 2004WO-US022830.  
 XX  
 PR 17-JUL-2003; 2003US-0487589P.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX  
 PI Gardella TJ;  
 XX  
 DR WPI; 2005-132386/14.  
 XX  
 PT New conformationally constrained parathyroid hormone analogs useful in  
 PT the treatment of e.g. hypercalcemia primary and hyperparathyroidism.  
 XX  
 PS Disclosure; SEQ ID NO 27; 49pp; English.  
 XX  
 The invention provides novel antagonists of the juxtaposition (J) domain  
 of the parathyroid hormone (PTH or parathormone) receptor. These  
 antagonists contain amino acid substitutions at selected positions in  
 truncated PTH and PTH-related polypeptide and function by selectively  
 binding the J domain of the receptor. The J domain is the region of the  
 receptor (PIR) that spans the seven transmembrane domain and the  
 extracellular loops. PIR polypeptide antagonists of the invention can be  
 used to treat conditions relating to PH/PIR hyperactivity, such as  
 hypercalcemia including malignant hypercalcemia (claimed), primary  
 hyperparathyroidism, and Jansen's chondrodysplasia. They can also be used  
 to identify other ligands (e.g. using a high-throughput screen) that bind  
 to PIR, such as small molecule PTH mimetic compounds, or for the  
 pharmacological analysis of PIR ligands for their selectivity, e.g. for  
 the J domain. The present sequence is that of rat PTH(1-21). PTH  
 derivatives of the invention contain changes in sequence relative to this  
 wild-type sequence. Note: this sequence is given as SEQ ID NO:27 on page  
 16 of the specification, but is different from the sequence given in SEQ  
 ID NO:27 in Figure 1 ADW88337.  
 XX  
 Sequence 21 AA;  
 Query Match 71.1%; Score 59; DB 9; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.022;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AVSEIQLMHNLG 12  
 DB 1 AVSEIQLMHNLG 12  
 RESULT 16  
 AAY98016  
 ID AAY98016 standard; peptide; 27 AA.  
 XX  
 AC AAY98016;  
 XX  
 DT 04-SEP-2000 (first entry)  
 XX  
 DE Human amino-terminal modified parathyroid hormone analogue # 7.  
 XX  
 KW Parathyroid hormone peptide; PTH; renal cell; osseous cell; human;  
 KW signal transduction; osteoporosis; amino-terminal modification;  
 KW bone disease; parathyroid hormone receptor; osteopenia;  
 KW hypoparathyroidism; fracture repair; hypercalcaemia; cancer; osteopathic.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT Modified-site 1





PI Bringhurst FR, Takasu H, Gardella TJ, Potts JT;  
 DR WPI; 2000-400076/34.  
 XX Novel biologically active peptide comprising a parathyroid hormone  
 PI peptide derivative, useful for treating osteoporosis.  
 XX  
 PS Disclosure; Page 68; 75pp; English.  
 XX  
 CC Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous  
 CC cells, initiating signal transduction. It has been identified that the  
 CC carboxyl terminal of PTH is important for PTH receptor binding, while the  
 CC amino terminal is important for signal transduction. Various PTH peptides  
 CC were produced with amino- and carboxy terminal modifications which had  
 CC varying PTH receptor activation properties and therefore downstream  
 CC signalling. Aberrant PTH activity has been implicated in a number of  
 CC disorders: osteoporosis, osteopaenia, hypoparathyroidism and  
 CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma  
 CC and a variety of cancers: breast, lung and prostate carcinoma, multiple  
 CC myeloma and epidermoid cancers of the head, neck and oesophagus. The  
 CC present sequence is a PTH peptide, with an Ala residue at position 1 and  
 CC an Arg residue at position 19. The Ala and Arg residues both improve  
 CC downstream signalling via phospholipase C (PLC) and ligand binding. The  
 CC present peptide may therefore be used as a PTH receptor agonist for the  
 CC treatment of the above mentioned disorders. In addition, the present  
 CC sequence would be suitable for fracture repair  
 XX  
 SQ Sequence 27 AA;

Query Match 71.1%; Score 59; DB 3; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.029;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AVSEIQLMHNLG 12  
 Db 1 AVSEIQLMHNLG 12

RESULT 19  
 ID AAY98048 standard; peptide; 28 AA.

XX AAY98048;  
 XX  
 DT 04-SEP-2000 (first entry)  
 XX Human parathyroid hormone peptide # 8.  
 DE  
 XX Human; parathyroid hormone; signal transduction; osteoporosis;  
 KW osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;  
 KW breast cancer; lung cancer; prostate cancer; multiple myeloma;  
 KW hypernephroma; head and neck epidermoid cancer; oesophagus cancer;  
 KW osteopathic; PTH.  
 XX  
 OS Homo sapiens.  
 XX WO200031266-A1.  
 FN 02-JUN-2000.

XX 24-NOV-1999; 99WO-US027863.  
 XX 25-NOV-1998; 98US-0109938P.  
 XX (GEO ) GEN HOSPITAL CORP.  
 XX Bringhurst FR, Takasu H, Gardella TJ, Potts JT;  
 XX WPI; 2000-400076/34.

XX Novel biologically active peptide comprising a parathyroid hormone  
 PT peptide derivative, useful for treating osteoporosis.  
 XX

PS Claim 8; Page 69; 75pp; English.  
 XX  
 CC Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous  
 CC cells, initiating signal transduction. It has been identified that the  
 CC carboxyl terminal of PTH is important for PTH receptor binding, while the  
 CC amino terminal is important for signal transduction. Various PTH peptides  
 CC were produced with amino- and carboxy terminal modifications which had  
 CC varying PTH receptor activation properties and therefore downstream  
 CC signalling. Aberrant PTH activity has been implicated in a number of  
 CC disorders: osteoporosis, osteopaenia, hypoparathyroidism and  
 CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma  
 CC and a variety of cancers: breast, lung and prostate carcinoma, multiple  
 CC myeloma and epidermoid cancers of the head, neck and oesophagus. The  
 CC present sequence is a PTH peptide, with an Ala residue at position 1 and  
 CC a Glu residue at position 19. The Ala residue improves downstream  
 CC signalling via phospholipase C (PLC), whereas the Glu residue reduces PLC  
 CC signalling and ligand binding. PTH peptides with a Arg residue at  
 CC position 19 have improved PLC signalling and ligand binding and so may be  
 CC used as a PTH receptor agonist for the treatment of the above mentioned  
 CC disorders and fracture repair  
 XX  
 SQ Sequence 28 AA;

Query Match 71.1%; Score 59; DB 3; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AVSEIQLMHNLG 12  
 Db 1 AVSEIQLMHNLG 12

RESULT 20  
 ID AAY98044 standard; peptide; 28 AA.

XX AAY98044;  
 XX  
 DT 04-SEP-2000 (first entry)  
 XX Human parathyroid hormone peptide # 4.  
 DE  
 XX Human; parathyroid hormone; signal transduction; osteoporosis;  
 KW osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;  
 KW breast cancer; lung cancer; prostate cancer; multiple myeloma;  
 KW hypernephroma; head and neck epidermoid cancer; oesophagus cancer;  
 KW osteopathic; PTH.  
 XX  
 OS Homo sapiens.  
 XX WO200031266-A1.  
 FN 02-JUN-2000.

XX 24-NOV-1999; 99WO-US027863.  
 XX 25-NOV-1998; 98US-0109938P.  
 XX (GEO ) GEN HOSPITAL CORP.  
 XX Bringhurst FR, Takasu H, Gardella TJ, Potts JT;  
 XX WPI; 2000-400076/34.

XX Novel biologically active peptide comprising a parathyroid hormone  
 PT peptide derivative, useful for treating osteoporosis.  
 XX  
 PS Claim 6; Page 68; 75pp; English.

XX Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous  
 CC cells, initiating signal transduction. It has been identified that the  
 CC carboxyl terminal of PTH is important for PTH receptor binding, while the  
 CC amino terminal is important for signal transduction. Various PTH peptides

CC were produces with amino- and carboxy terminal modifications which had  
CC varying PTH receptor activation properties and therefore downstream  
CC signalling. Aberrant PTH activity has been implicated in a number of  
CC disorders: osteoporosis, osteopaenia, hypoparathyroidism and  
CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma  
CC and a variety of cancers: breast, lung and prostate carcinoma, multiple  
CC myeloma and epidermoid cancers of the head, neck and oesophagus. The  
CC present sequence is a PTH peptide, with an Ala residue at position 1 and  
CC an Arg residue at position 19. The Ala and Arg residues both improve  
CC downstream signalling via phospholipase C (PLC) and ligand binding. The  
CC present peptide may therefore be used as a PTH receptor agonist for the  
CC treatment of the above mentioned disorders. In addition, the present  
CC sequence would be suitable for fracture repair  
XX  
SQ Sequence 28 AA;

Query Match 71.1%; Score 59; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. NO. 0.03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 AVSEIQLMHNIG 12  
| | | | | | | | | |  
Db 1 AVSEIQLMHNIG 12

Search completed: November 21, 2005, 16:38:10  
Job time : 189 secs

1. Page Blank (uspto)

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OM protein - protein search, using sw model

Run on: November 21, 2005, 16:30:49 ; Search time 38 Seconds

(without alignments)  
40.512 Million cell updates/sec

Title: SEQ-NEW

Perfect score: 83

Sequence: 1 avseiqmhnlgggg 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	71.1	115	2 A05091	parathyroid hormon
2	58	69.9	105	2 I51851	parathyroid hormon
3	56	67.5	115	1 PTHU	parathyroid hormon
4	56	67.5	115	1 PTPG	parathyroid hormon
5	55	66.3	115	1 PTBO	parathyroid hormon
6	53	63.9	119	2 A34937	parathyroid hormon
7	52	62.7	115	2 JC4202	parathyroid hormon
8	47	56.6	383	2 G69205	lipid-transfer pro
9	46	55.4	448	2 T43624	tubulin beta chain
10	46	55.4	448	2 A21649	tubulin beta chain
11	46	55.4	448	2 T40019	tubulin beta chain
12	46	55.4	456	2 S55661	hypothetical prote
13	45	54.2	395	2 S70637	tubulin beta chain
14	45	54.2	420	2 T22718	hypothetical prote
15	45	54.2	446	2 A27424	tubulin beta chain
16	45	54.2	450	2 S37177	tubulin beta chain
17	45	54.2	962	2 A84497	probable retroelem
18	44	53.0	196	2 E84638	probable RS2p22 sp
19	44	53.0	267	2 B82694	copper homeostasis
20	44	53.0	305	2 T04621	hypothetical prote
21	44	53.0	447	2 S17729	tubulin beta chain
22	44	53.0	447	2 S17730	tubulin beta chain
23	44	53.0	556	2 T06126	calcium-dependent
24	43	51.8	321	2 B25437	tubulin beta-2 cha
25	43	51.8	360	2 S18458	tubulin beta chain
26	43	51.8	437	2 I38369	beta-tubulin - hum
27	43	51.8	441	2 S05956	tubulin beta-2 cha
28	43	51.8	441	2 S45071	tubulin beta chain
29	43	51.8	443	2 S05968	tubulin beta-2 cha

30	43	51.8	444	1 UBHU5B	tubulin beta chain
31	43	51.8	444	2 D25437	tubulin beta-4 cha
32	43	51.8	444	2 S01713	tubulin beta-7 cha
33	43	51.8	444	2 A26561	tubulin beta chain
34	43	51.8	444	2 S18457	tubulin beta chain
35	43	51.8	444	2 S18456	tubulin beta chain
36	43	51.8	444	2 E25437	tubulin beta-5 cha
37	43	51.8	445	1 UBCHB	tubulin beta chain
38	43	51.8	445	1 UBRGB	tubulin beta chain
39	43	51.8	445	2 A25113	tubulin beta chain
40	43	51.8	445	2 B45794	tubulin beta-3 cha
41	43	51.8	445	2 A24701	tubulin beta chain
42	43	51.8	445	2 I50435	beta-tubulin - hum
43	43	51.8	445	2 I38370	tubulin beta chain
44	43	51.8	445	2 S37144	tubulin beta-3 cha
45	43	51.8	445	2 C25437	tubulin beta chain
46	43	51.8	445	2 A54515	tubulin beta chain
47	43	51.8	445	2 T08726	tubulin beta-2 cha
48	43	51.8	446	2 A27810	tubulin beta-5 cha
49	43	51.8	446	2 B27554	neural class-II be
50	43	51.8	446	2 A48407	tubulin beta chain
51	43	51.8	447	2 S05429	beta-tubulin - nem
52	43	51.8	448	2 A45603	tubulin beta chain
53	43	51.8	448	2 S62125	beta-tubulin isoty
54	43	51.8	448	2 S53776	tubulin beta-4 cha
55	43	51.8	449	2 A29161	hypothetical prote
56	43	51.8	449	2 T23201	tubulin beta-1 cha
57	43	51.8	450	2 A25437	hypothetical prote
58	43	51.8	450	2 T19788	hypothetical prote
59	43	51.8	452	2 T20194	hypothetical prote
60	43	51.8	453	2 S18597	tubulin beta chain
61	43	51.8	454	2 B27810	tubulin beta-3 cha
62	43	51.8	488	2 G65216	hypothetical 53.4
63	43	51.8	589	2 T19216	hypothetical prote
64	43	51.8	611	2 T19217	hypothetical prote
65	43	51.8	2174	2 E95965	hypothetical glyci
66	42	50.6	293	2 F75380	hypothetical prote
67	42	50.6	323	2 S20099	transforming prote
68	42	50.6	378	2 S20172	myoglobin - Japane
69	42	50.6	447	2 S43426	tubulin beta chain
70	42	50.6	1196	2 H85061	hypothetical prote
71	41	49.4	173	2 S53050	RNA binding protei
72	41	49.4	204	2 S02532	tubulin beta-1 cha
73	41	49.4	262	2 T51409	MADS box protein A
74	41	49.4	274	2 JC4053	chitinase [EC 3.2.
75	41	49.4	282	2 A25342	tubulin beta chain
76	41	49.4	342	1 TVMVN9	protein kinase (EC
77	41	49.4	354	1 TVMVMT	protein kinase (EC
78	41	49.4	374	1 TVMVHT	protein kinase (EC
79	41	49.4	374	1 TVMVMT	protein kinase (EC
80	41	49.4	376	1 TVMV1M	protein kinase (EC
81	41	49.4	390	1 TVMSM	tubulin beta subun
82	41	49.4	441	2 E90136	tubulin beta chain
83	41	49.4	442	1 UBUTB	tubulin beta chain
84	41	49.4	442	2 S25182	tubulin beta-1 cha
85	41	49.4	442	2 S00683	tubulin beta-1 cha
86	41	49.4	442	2 S20908	tubulin beta chain
87	41	49.4	442	2 S05496	tubulin beta chain
88	41	49.4	443	2 S01769	tubulin beta-2 cha
89	41	49.4	443	2 S01768	tubulin beta-1 cha
90	41	49.4	443	2 S41470	tubulin beta chain
91	41	49.4	444	2 A5615	beta-tubulin - Pla
92	41	49.4	444	2 S31400	tubulin beta chain
93	41	49.4	444	2 A35885	tubulin beta chain
94	41	49.4	444	2 T18683	hypothetical prote
95	41	49.4	444	2 S35191	tubulin beta-1 cha
96	41	49.4	444	2 T15310	hypothetical prote
97	41	49.4	445	1 UBZOF	tubulin beta chain
98	41	49.4	445	2 S00743	tubulin beta chain
99	41	49.4	445	2 JA0048	tubulin beta-1 cha
100	41	49.4	445	2 JN0499	tubulin beta chain

## ALIGNMENTS

```

RESULT 1
A05091
parathyroid hormone precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C:Accession: A05091; A26806
R:Schmeizer, H.J.; Gross, G.; Widera, G.; Mayer, H.
R:Heinrich, G.; Krombach, H.M.; Potts Jr., J.T.; Habener, J.F.
J Biol. Chem. 259, 3320-3329, 1984
A:Reference number: A05091; MUID:164135846; PMID:6321505
A:Accession: A05091
A:Molecule type: DNA
A:Residues: 1-115 <HEI>
A:Cross-references: UNIPROT:P04089; UNIPARC:UPI000013290C; GB:K01268; NID:G206483; PIDN:
R:Schmeizer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A:Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hor
A:Reference number: A26806; MUID:87316938; PMID:3628009
A:Accession: A26806
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-115 <SCH>
A:Cross-references: UNIPARC:UPI000013290C; GB:X05721; GB:Y00409; NID:G56002; PIDN:CAA291
C:Genetics:
A:Introns: 29/3
C:Superfamily: parathyroid hormone; parathyroid hormone homology
F:30-64/Domain: parathyroid hormone homology <PTH>

Query Match 71.1%; Score 59; DB 2; Length 115;
Best Local Similarity 100.0%; Pred No. 0.022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNIG 12
DB 32 AVSEIQLMHNIG 43

RESULT 2
I51851
parathyroid hormone - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I51851
R:Schmeizer, H.
Adv. Gene Technol. 21, 228-229, 1984
A:Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.
A:Reference number: I51851
A:Accession: I51851
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-105 <RES>
A:Cross-references: UNIPARC:UPI0000170AE0; GB:M54875; NID:G601932; PIDN:AAA57156.1; PID:
C:Genetics:
A:Gene: PTH
C:Superfamily: parathyroid hormone; parathyroid hormone homology
F:20-54/Domain: parathyroid hormone homology <PTH>

Query Match 69.9%; Score 58; DB 2; Length 105;
Best Local Similarity 91.7%; Pred. No. 0.029;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNIG 12
DB 22 AISEIQLMHNIG 33

RESULT 3
PTHU
parathyroid hormone precursor [validated] - human
N:Alternate names: preproparathyroid hormone

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C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence revision 19-Jan-1996 #text change 09-Jul-2004
C:Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90426; A94410; I383
R:Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983
A:Title: Nucleotide sequence of the human parathyroid hormone gene.
A:Reference number: A19339; MUID:83169834; PMID:6220408
A:Accession: A19339
A:Molecule type: DNA
A:Residues: 1-115 <VAS>
A:Cross-references: UNIPROT:P01270; UNIPARC:UPI000013290A; GB:J00301; NID:G190702; PIDN:
R:Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.
Biochem. Biophys. Res. Commun. 194, 375-381, 1994
A:Title: Purification of meprin from human kidney and its role in parathyroid hormone deg
A:Reference number: S53790; MUID:95225986; PMID:7710697
A:Accession: S53790
A:Molecule type: protein
A:Residues: X'33, X'35-46; 65-84; 105-110 <YAM>
A:Cross-references: UNIPARC:UPI00001734E1; UNIPARC:UPI00001734E2; UNIPARC:UPI00001734E3
A:Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also occur
R:Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.
Nature 249, 155-157, 1974
A:Title: Structural analysis of human preproparathyroid hormone by a new microsequencing ap
A:Reference number: A93169; MUID:74174967; PMID:4833516
A:Accession: A93169
A:Molecule type: protein
A:Residues: 26-37 <JAC>
A:Cross-references: UNIPARC:UPI00001734E4
R:Olstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik, V.T.
Eur. J. Biochem. 205, 311-319, 1992
A:Title: Isolation and characterization of two biologically active O-glycosylated forms c
ation.
A:Reference number: S21199; MUID:92209518; PMID:1555591
A:Accession: S21199
A:Molecule type: protein
A:Residues: 32-114, N' <OLS>
A:Cross-references: UNIPARC:UPI00001734E5
A:Note: Cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylation;
R:Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L.H.;
Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974
A:Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyroid h
A:Reference number: A93789; MUID:74111656; PMID:4521809
A:Accession: A93789
A:Molecule type: protein
A:Residues: 32-68 <NIA>
A:Cross-references: UNIPARC:UPI000002DA05
R:Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D.
Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972
A:Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal residues i-
A:Reference number: A93783; MUID:73070429; PMID:4509319
A:Accession: A93783
A:Molecule type: protein
A:Residues: 32-52, Q', 54-58, K', 60, L', 62-65 <BRE>
A:Cross-references: UNIPARC:UPI00001734E6
A:Note: this sequence was determined by sequenator and mass spectroscopic identification
R:Keutmann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 14, 1842-1847, 1975
A:Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone.
A:Reference number: A90387; MUID:75146516; PMID:1125201
A:Accession: A90387
A:Molecule type: protein
A:Residues: 52-75 <KE3>
A:Cross-references: UNIPARC:UPI00001734E7
R:Keutmann, H.T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 17, 5723-5725, 1978
A:Title: Complete amino acid sequence of human parathyroid hormone.
A:Reference number: A90426; MUID:79082855; PMID:728431
A:Accession: A90426
A:Molecule type: protein
A:Residues: 61-106, D', 108-115 <KEU>
A:Cross-references: UNIPARC:UPI00001734E8
R:Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.H.
in Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9-11

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A;Reference number: A94410  
A;Accession: A94410  
A;Molecule type: protein  
A;Residues: 75-100 <KE2>  
A;Cross-references: UNIPARC:UPI00001734E9  
R;Tregear, G.W.; van Riettschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J.  
Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974  
A;Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of human parathyroid hormone  
A;Reference number: A91660; MUID:7509220; PMID:4474131  
A;Contents: annotation; synthesis of residues 32-65  
A;Note: the biologically active amino-terminal 34 residues of parathyroid hormone were synthesized at renal adenylate cyclase assay and with the bovine hormone's active region in the child  
R;Andraetta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, B.; Riniker, B.; Rittel, Hely. Chim. Acta 56, 470-473, 1973  
A;Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.  
A;Reference number: A91635; MUID:73227467; PMID:4721748  
A;Contents: annotation; synthesis of residues 32-65  
A;Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined into chyroparathyroidectomized rats caused a distinct increase in plasma calcium level  
R;Hendy, G.N.; Kronenberg, H.M.; Potts, J.T.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981  
A;Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.  
A;Reference number: I38342; MUID:82150870; PMID:6950381  
A;Accession: I38342  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-115 <RES>  
A;Cross-references: UNIPARC:UPI000013290A; EMBL:V00597; NID:g37143; PIDN:CAA23843.1; PIDN:CAA23439.1  
A;Genes: GDB:PTH  
A;Cross-references: GDB:119522; OMIM:168450  
A;Map position: 11p15.2-11p15.1  
A;Introns: 29/2  
A;Note: the first intron occurs before the initiator codon  
C;Function:  
A;Description: factor in homeostatic control of plasma calcium and phosphate; released by parathyroid hormone precursor - pig  
C;Superfamily: parathyroid hormone; parathyroid hormone homology  
C;Keywords: calcium; hormone; parathyroid gland; plasma  
F;1-25/Domain: signal sequence #status predicted <SIG>  
F;26-31/Domain: propeptide #status experimental <PRO>  
F;30-64/Domain: parathyroid hormone homology <PTH>  
F;32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 67.5%; Score 56; DB 1; Length 115;  
Best Local Similarity 91.7%; Pred. No. 0.067;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNILG 12  
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Db 32 SVSEIQLMHNILG 43

RESULT 4  
PTPG  
Parathyroid hormone precursor - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 24-Apr-1984 #sequence\_revision 12-Apr-1996 #text\_change 09-Jul-2004  
C;Accession: B26806; A90390; A90376; A01535  
R;Schmelzer, H.J.; Gross, G.; Wiedera, G.; Mayer, H.  
Nucleic Acids Res. 15, 6740, 1987  
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone  
A;Reference number: A26806; MUID:87316938; PMID:3628009  
A;Accession: B26806  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-115 <SCH>  
A;Cross-references: UNIPROT:P01269; UNIPARC:UPI000013290B; GB:X05722; GB:Y00409; NID:g18  
R;Chu, L.L.H.; Huang, W.Y.; Littlelike, E.T.; Hamilton, J.W.; Cohn, D.V.  
Biochemistry 14, 3631-3635, 1975  
A;Title: Porcine preparathyroid hormone. Identification, biosynthesis, and partial amino acid sequence  
A;Reference number: A90390; MUID:76018954; PMID:1164500  
A;Accession: A90390

A;Molecule type: protein  
A;Residues: 26-115 <CHU>  
A;Cross-references: UNIPARC:UPI00001592DF  
R;Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr., J.  
Biochemistry 13, 1994-1999, 1974  
A;Title: The amino acid sequence of porcine parathyroid hormone.  
A;Reference number: A90376; MUID:74253317; PMID:4840833  
A;Accession: A90376  
A;Molecule type: protein  
A;Residues: 32-109 <SAU>  
A;Cross-references: UNIPARC:UPI00001734E0  
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littlelike, T.; Arnaud, C.D.  
Am. J. Med. 56, 759-766, 1974  
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone  
A;Reference number: A90030; MUID:74173303; PMID:4598526  
A;Contents: annotation  
C;Superfamily: parathyroid hormone; parathyroid hormone homology  
C;Keywords: calcium; hormone; parathyroid gland  
F;1-25/Domain: signal sequence #status predicted <SIG>  
F;26-31/Domain: propeptide #status experimental <PRO>  
F;30-64/Domain: parathyroid hormone homology <PTH>  
F;32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 67.5%; Score 56; DB 1; Length 115;  
Best Local Similarity 91.7%; Pred. No. 0.067;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNILG 12  
:|||||  
Db 32 SVSEIQLMHNILG 43

RESULT 5  
PTPG  
Parathyroid hormone precursor - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 09-Jul-2004  
C;Accession: A24949; A93835; A93793; A91648; A93773; I45975; I45976; A01534  
R;Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.  
Gene 28, 319-329, 1984  
A;Title: Isolation and complete nucleotide sequence of the gene for bovine parathyroid hormone  
A;Reference number: A24949; MUID:84262483; PMID:6086460  
A;Accession: A24949  
A;Molecule type: DNA  
A;Residues: 1-115 <WEA>  
A;Cross-references: UNIPROT:P01268; UNIPARC:UPI0000132907; GB:K01938  
R;Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; Potts Jr., J.  
Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979  
A;Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid hormone  
A;Reference number: A93835; MUID:80056617; PMID:388425  
A;Accession: A93835  
A;Molecule type: DNA  
A;Residues: 1-115 <KRO>  
A;Cross-references: UNIPARC:UPI0000132907; GB:V00106; GB:J00023; NID:984; PIDN:CAA23439.1  
A;Note: the authors translated the codon GAA for residue 50 as Gly  
R;Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn, D.V.  
Proc. Natl. Acad. Sci. U.S.A. 71, 653-656, 1974  
A;Title: The N-terminal amino-acid sequence of bovine preproparathyroid hormone.  
A;Reference number: A93793; MUID:74142666; PMID:4522780  
A;Accession: A93793  
A;Molecule type: protein  
A;Residues: 26-115 <HAM>  
A;Cross-references: UNIPARC:UPI00001734DF  
R;Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; Dawson, B.F.; Aurbach, G.D.; Potl  
Hoppe-Seyler's Z. Physiol. Chem. 351, 1586-1588, 1970  
A;Title: The amino acid sequence of bovine parathyroid hormone I.  
A;Reference number: A91648; MUID:71076162; PMID:5531031  
A;Accession: A91648  
A;Molecule type: protein  
A;Residues: 32-115 <NIA>  
A;Cross-references: UNIPARC:UPI000000473E4  
R;Brewer Jr., H.B.; Ronan, R.  
Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970

A:Title: Bovine parathyroid hormone: amino acid sequence.  
A:Reference number: A93773; MUID:71063634; PMID:5275384  
A:Accession: A93773  
A:Molecule type: protein  
A:Residues: 32-115 <BRE>  
A:Cross-references: UNIPARC:UPI00000473E4  
R:Potter Jr., J.T.; Tegear, G.W.; Keutmann, H.T.; Niall, H.D.; Sauer, R.; Deftos, L.J.; Proc. Natl. Acad. Sci. U.S.A. 68, 63-67, 1971  
A:Title: Synthesis of a biologically active N-terminal tetracontapeptide of parathyroid hormone.  
A:Reference number: A93776; MUID:71091588; PMID:4322265  
A:Contents: annotation; synthesis of residues 32-65  
A:Note: The synthetic peptide was active in vivo and in vitro  
R:Brown Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D. Am. J. Med. 56, 759-766, 1974  
A:Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone.  
A:Reference number: A90030; MUID:74173303; PMID:4598526  
A:Contents: annotation  
R:Weaver, C.A.; Gordon, D.F. Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981  
A:Title: Introduction by molecular cloning of artifactual inverted sequences at the 5' end of the parathyroid hormone gene.  
A:Reference number: I45975; MUID:82037785; PMID:6170060  
A:Accession: I45975  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-115 <WE2>  
A:Cross-references: UNIPARC:UPI0000132907; GB:J00024; NID:g163642; PIDN:AAA30747.1; PID:6170060  
R:Weaver, C.A.; Gordon, D.F. Mol. Cell. Endocrinol. 28, 411-424, 1982  
A:Title: Nucleotide sequence of bovine parathyroid hormone mRNA.  
A:Reference number: I45976; MUID:83105964; PMID:6185374  
A:Accession: I45976  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-115 <WE3>  
A:Cross-references: UNIPARC:UPI0000132907; GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:6185374  
C:Genetics: PTH  
A:Gene: PTH  
A:Introns: 29/2  
A:Superfamily: parathyroid hormone; parathyroid hormone homology  
C:Keywords: hormone  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-31/Product: parathyroid hormone #status experimental <PMAT>  
F:32-115/Domain: propeptide #status experimental <PRO>  
F:30-64/Domain: parathyroid hormone homology <PTH>  
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Best Local Similarity 91.7%; Pred. No. 0.096; Mismatches 1; Indels 0; Gaps 0;  
Matches 11; Conservative 0;  
QY 1 AVSEIQFMHNLG 12  
DB 32 AVSEIQFMHNLG 43  
RESULT 6  
A:Accession: A93773  
parathyroid hormone precursor - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
A:Reference number: A34937; MUID:89219100; PMID:2710135  
A:Title: Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyroid hormone.  
A:Accession: A34937  
A:Molecule type: mRNA  
A:Residues: 1-119 <RUS>  
A:Cross-references: UNIPARC:UPI0000132909; GB:M1604; NID:g212767; PIDN:2710135  
R:Khoshla, S.; Demay, M.; Pines, M.; Hurwitz, S.; Potts, J.T. J. Bone Miner. Res. 3, 689-698, 1988  
A:Title: Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone.  
A:Reference number: I50411; MUID:89284968; PMID:3251402

A:Accession: I50411  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-119 <KHO>  
A:Cross-references: UNIPARC:UPI0000132909; GB:M36522; NID:g212591; PIDN:AAB02866.1; PID:5275384  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-31/Domain: propeptide #status predicted <PRO>  
F:30-64/Domain: parathyroid hormone homology <PTH>  
F:32-119/Product: parathyroid hormone #status predicted <MAT>  
Query Match 63.9%; Score 53; DB 2; Length 119;  
Best Local Similarity 83.3%; Pred. No. 0.21; Mismatches 2; Indels 0; Gaps 0;  
Matches 10; Conservative 2;  
QY 1 AVSEIQFMHNLG 12  
DB 32 AVSEIQFMHNLG 43  
RESULT 7  
parathyroid hormone precursor - dog  
C:Species: Canis lupus familiaris (dog)  
C:Date: 10-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 09-Jul-2004  
A:Reference number: JC4202  
R:Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, C.C. Gene 160, 241-243, 1995  
A:Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein and its mRNA.  
A:Reference number: JC4201; MUID:95369696; PMID:7642102  
A:Accession: JC4202  
A:Molecule type: mRNA  
A:Residues: 1-115 <ROS>  
A:Cross-references: UNIPROT:P52212; UNIPARC:UPI0000132908; GB:U15662; NID:g558915; PIDN:7642102  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:30-64/Domain: parathyroid hormone homology <PTH>  
F:32-115/Product: parathyroid hormone #status predicted <MAT>  
Query Match 62.7%; Score 52; DB 2; Length 115;  
Best Local Similarity 83.3%; Pred. No. 0.29; Mismatches 1; Indels 0; Gaps 0;  
Matches 10; Conservative 1;  
QY 1 AVSEIQFMHNLG 12  
DB 32 AVSEIQFMHNLG 43  
RESULT 8  
lipid-transfer protein (sterol or nonspecific) - Methanobacterium thermoautotrophicum (strain ATCC 35061) (Delta H)  
C:Species: Methanobacterium thermoautotrophicum  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
A:Reference number: G69205  
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; F. Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; K. S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997  
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: function and organization of the genome.  
A:Reference number: A69000; MUID:98037514; PMID:9371463  
A:Accession: G69205  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-383 <MTH>  
A:Cross-references: UNIPROT:Q26884; UNIPARC:UPI00000664E4; GB:AE000857; GB:AE000666; NID:9371463  
C:Genetics: Delta H  
A:Gene: MTH793  
Query Match 56.6%; Score 47; DB 2; Length 383;  
Best Local Similarity 57.1%; Pred. No. 6.9; Mismatches 3; Indels 0; Gaps 0;  
Matches 8; Conservative 3;



QY 3 SEIQLMHNLGGGG 16  
: : : : :  
Db 361 AEIGTMHNLGGTG 374

RESULT 9  
T43624  
beta tubulin, temperature sensitive - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T43624  
R;Radcliffe, P.; Hirata, D.; Childs, D.; Vardy, L.; Toda, T.  
Mol. Biol. Cell 9, 1757-1771, 1998  
A;Title: Identification of novel temperature-sensitive lethal alleles in essential beta-tubulin  
A;Reference number: 222579; MUID:98324923; PMID:9658169  
A;Accession: T43624  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-448 <RAD>  
A;Cross-references: UNIPROT:P05219; UNIPARC:UPI0000168807; EMBL:AF042828; PIDN:AAC21455-1  
A;Experimental source: strain 972  
C;Genetics:  
A;Gene: nda3  
A;Map position: 2  
A;Introns: 4/3; 21/2; 35/3; 349/1  
C;Superfamily: tubulin

Query Match 55.4%; Score 46; DB 2; Length 448;  
Best Local Similarity 56.2%; Pred. No. 12;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLGGGG 16  
: : : : :  
Db 129 ALQGFQLTHSLGGGTG 144

RESULT 10  
A21649  
tubulin beta chain - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 09-Jul-2004  
C;Accession: A21649  
R;Hiraoka, Y.; Toda, T.; Yanagida, M.  
Cell 39, 349-358, 1984  
A;Title: The NDA3 gene of fission yeast encodes beta-tubulin: a cold-sensitive nda3 mutant  
A;Reference number: A21649; MUID:85048945; PMID:6094012  
A;Accession: A21649  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-448 <HIR>  
A;Cross-references: UNIPROT:P05219; UNIPARC:UPI00001691C0; GB:M10347; NID:gl73522; PIDN:  
C;Superfamily: tubulin

Query Match 55.4%; Score 46; DB 2; Length 448;  
Best Local Similarity 56.2%; Pred. No. 12;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLGGGG 16  
: : : : :  
Db 129 ALQGFQLTHSLGGGTG 144

RESULT 11  
T40019  
beta tubulin - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T40019; T43623  
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.  
submitted to the EMBL Data Library, September 1998  
A;Reference number: 221899  
A;Accession: T40019

A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-448 <WOO>  
A;Cross-references: UNIPROT:P05219; UNIPARC:UPI0000136A39; EMBL:AL031743; PIDN:CAA21099-1  
A;Experimental source: strain 972h; Cosmid C36H8  
R;Radcliffe, P.; Hirata, D.; Childs, D.; Vardy, L.; Toda, T.  
Mol. Biol. Cell 9, 1757-1771, 1998  
A;Title: Identification of novel temperature-sensitive lethal alleles in essential beta-tubulin  
A;Reference number: 222579; MUID:98324923; PMID:9658169  
A;Accession: T43623  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-448 <RAD>  
A;Cross-references: UNIPARC:UPI0000136A39; EMBL:AF042827; PIDN:AAC21454-1  
A;Experimental source: strain 972  
C;Genetics:  
A;Gene: nda3; SPBC26H8.07c  
A;Map position: 2  
A;Introns: 4/3; 21/2; 35/3; 349/1  
C;Superfamily: tubulin

Query Match 55.4%; Score 46; DB 2; Length 448;  
Best Local Similarity 56.2%; Pred. No. 12;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLGGGG 16  
: : : : :  
Db 129 ALQGFQLTHSLGGGTG 144

RESULT 12  
S55661  
hypothetical protein 66 - equine herpesvirus 2  
C;Species: equine herpesvirus 2  
C;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S55661  
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.  
J. Mol. Biol. 249, 520-528, 1995  
A;Title: The DNA sequence of equine herpesvirus 2.  
A;Reference number: S55594; MUID:95302501; PMID:7783207  
A;Accession: S55661  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-456 <TEL>  
A;Cross-references: UNIPROT:Q66668; UNIPARC:UPI00000F0F2B; GB:U20824; NID:9695172; PIDN:  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995

Query Match 55.4%; Score 46; DB 2; Length 456;  
Best Local Similarity 63.6%; Pred. No. 12;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 QLMHNLGGGG 16  
: : : : :  
Db 8 EIFHRLGGGG 18

RESULT 13  
S70637  
tubulin beta chain - Hexamita sp. (strain ATCC 50330) (fragment)  
C;Species: Hexamita sp.  
A;Variety: ATCC 50330  
C;Date: 21-Apr-1997 #sequence\_revision 21-Apr-1997 #text\_change 07-Dec-1999  
C;Accession: S70637  
R;Keeling, P.J.; Doolittle, W.F.  
EMBO J. 15, 2285-2290, 1996  
A;Title: A non-canonical genetic code in an early diverging eukaryotic lineage.  
A;Reference number: S70634; MUID:96208514; PMID:8641293  
A;Accession: S70637  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-395 <KEE>  
A;Cross-references: UNIPARC:UPI000007A51C; EMBL:U29441; NID:gl322213; PIDN:AAC47210-1; P  
A;Experimental source: ATCC 50330

A>Note: the sequence of residues 388-395 and the corresponding nucleic acid sequence are  
C:Genetics:  
A:Genetic code: SGC5  
C:Superfamily: tubulin

Query Match 54.2%; Score 45; DB 2; Length 395;  
Best Local Similarity 72.7%; Pred. No. 15;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 6 QLMHNLGGGGG 16  
DB 119 QLVHSLGGGTG 129

RESULT 14  
T22718  
hypothetical protein T04H1.9 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T22718; T24481  
R:Harris, B.  
submitted to the EMBL Data Library, August 1996  
A:Reference number: Z19604  
A:Accession: T22718  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-420 <WIL>  
A:Cross-references: UNIPROT:Q20823; UNIPARC:UPI0000061142; EMBL:Z78198; PIDN:CAB01575.1;  
A:Experimental source: clone F55C5  
R:Harris, B.  
submitted to the EMBL Data Library, August 1996  
A:Reference number: Z19696  
A:Accession: T24481  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-420 <WIL>  
A:Cross-references: UNIPARC:UPI0000061142; EMBL:Z78200; PIDN:CAB01587.1; GSPDB:GN00023;  
A:Experimental source: clone T04H1  
C:Genetics:  
A:Gene: CESP:T04H1.9  
A:Map position: 5  
A:Introns: 56/1; 120/1; 224/1; 379/1  
C:Superfamily: tubulin

Query Match 54.2%; Score 45; DB 2; Length 420;  
Best Local Similarity 72.7%; Pred. No. 16;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 6 QLMHNLGGGGG 16  
DB 134 QLVHSLGGGTG 144

RESULT 15  
A27424  
tubulin beta chain - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
C:Accession: A27424  
R:Murphy, D.B.; Wallis, K.T.; Machlin, P.S.; Rattie III, H.; Cleveland, D.W.  
J. Biol. Chem. 262, 14305-14312, 1987  
A:Title: The sequence and expression of the divergent beta-tubulin in chicken erythrocyte  
A:Reference number: A27424; MUID:88007687; PMID:2888766  
A:Accession: A27424  
A:Molecule type: mRNA  
A:Residues: 1-446 <MUR>  
A:Cross-references: UNIPROT:P09207; UNIPARC:UPI0000136A03; GB:J02828; NID:G212833; PIDN:  
C:Superfamily: tubulin  
C:Keywords: microtubule

Query Match 54.2%; Score 45; DB 2; Length 446;  
Best Local Similarity 72.7%; Pred. No. 17;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 QLMHNLGGGGG 16  
DB 134 QLVHSLGGGTG 144

RESULT 16  
S37177  
tubulin beta chain - silkworm  
C:Species: Bombyx mori (silkworm)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S37177  
R:Mita, K.  
submitted to the EMBL Data Library, September 1993  
A:Reference number: S37177  
A:Accession: S37177  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-450 <MIT>  
A:Cross-references: UNIPROT:P41385; UNIPARC:UPI0000136A12; EMBL:X74951; NID:G402173; PIDN:  
C:Superfamily: tubulin

Query Match 54.2%; Score 45; DB 2; Length 450;  
Best Local Similarity 72.7%; Pred. No. 17;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 QLMHNLGGGGG 16  
DB 134 QLVHSLGGGTG 144

RESULT 17  
A84497  
probable retroelasm pol polyprotein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: A84497  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Nuss, D.; Nietman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: A84497  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-962 <STO>  
A:Cross-references: UNIPROT:Q9ZQM1; UNIPARC:UPI00000A892C; GB:AE002093; NID:G4263654; PII  
C:Genetics:  
A:Gene: At2g11230  
A:Map position: 2

Query Match 54.2%; Score 45; DB 2; Length 962;  
Best Local Similarity 66.7%; Pred. No. 39;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 QLMHNLGGGGG 16  
DB 656 VOLTHRLGGRGG 667

RESULT 18  
E84638  
probable RSP22 splicing factor [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: E84638  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Nuss, D.; Nietman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: B84638  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-196 <STO>  
A;Cross-references: UNIPROT:Q9SJA6; UNIPARC:UPI000000C588; GB:AE002093; NID:g4572679; PI  
C;Genetics:  
A;Gene: At2g24590  
A;Map position: 2  
C;Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology

Query Match 53.0%; Score 44; DB 2; Length 196;  
Best Local Similarity 58.3%; Pred. No. 10;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 5 IQLMHNLTGGGG 16  
DB 66 VEQSHNRGGGG 77

RESULT 19  
B82694  
copper homeostasis protein XF1341 [imported] - Xylella fastidiosa (strain 9a5c)  
C;Species: Xylella fastidiosa  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: B82694  
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A;Reference number: A82515; MUID:20365717; PMID:10910347  
A;Note: for a complete list of authors see reference number A59328 below  
A;Accession: B82694  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-267 <SIM>  
A;Cross-references: UNIPROT:Q9PDN8; UNIPARC:UPI000000C26D0; GB:AE003966; GB:AE003849; NID  
A;Experimental source: strain 9a5c  
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincan, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B  
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A;Reference number: A59328  
A;Contents: annotation  
C;Genetics:  
A;Gene: XF1341

Query Match 53.0%; Score 44; DB 2; Length 267;  
Best Local Similarity 63.6%; Pred. No. 14;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 5 IQLMHNLTGGGG 15  
DB 49 VELCHLGGGG 59

RESULT 20  
T04621  
hypothetical protein F2009.190 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: T04621  
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X  
submitted to the Protein Sequence Database, October 1998  
A;Reference number: Z15380  
A;Accession: T04621  
A;Molecule type: DNA

A;Residues: 1-305 <BEV>  
A;Cross-references: UNIPROT:O49459; UNIPARC:UPI000000A2285; EMBL:AL021749  
A;Experimental source: cultivar Columbia; BAC clone F2009  
C;Genetics:  
A;Map position: 4  
A;Introns: 50/3; 114/1  
A;Note: F2009.190

Query Match 53.0%; Score 44; DB 2; Length 305;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 8 MHNLTGGGG 16  
DB 241 LHGLGGGG 249

Search completed: November 21, 2005, 16:38:53  
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 16:31:04 ; Search time 234 Seconds  
(without alignments)  
48.241 Million cell updates/sec

Title: SEQ-NEW

Perfect score: 83

Sequence: 1 aveeiqlmhnlggggg 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot 05.80:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	71.1	31	Q91Y90 PERMA	Q91Y90 peromyscus
2	59	71.1	31	Q91Y91 PERPL	Q91Y91 peromyscus
3	59	71.1	105	Q80W22 RAT	Q80W22 rattus norv
4	59	71.1	115	PTHY RAT	P04089 rattus norv
5	59	71.1	115	Q92016 MOUSE	Q92016 mus musculus
6	56	67.5	86	Q9N1V0 HORSE	P01270 equus caball
7	56	67.5	115	PTHY HUMAN	P01270 homo sapien
8	56	67.5	115	PTHY MACFA	Q9XT35 macaca fasc
9	56	67.5	115	PTHY PIG	P01269 sus scrofa
10	56	67.5	115	Q4VB48 HUMAN	Q4VB48 homo sapien
11	55	66.3	102	Q5TL21 BRARE	Q5TL21 brachydanio
12	55	66.3	102	Q6WQ25 BRARE	Q6WQ25 brachydanio
13	55	66.3	115	PTHY BOVIN	P01268 bos taurus
14	53	63.9	119	PTHY CHICK	P15743 gallus gall
15	52	62.7	115	PTHY CANFA	P52212 canis famil
16	52	62.7	115	PTHY FELCA	Q9GL67 felis silve
17	50	60.2	394	Q8TV11 METKA	Q8TV11 methanopyru
18	49	59.0	885	Q5YGS9 DICDI	Q5YGS9 dictyosteli
19	48	57.8	140	Q5SX26 MOUSE	Q5SX26 mus musculus
20	48	57.8	190	Q5SX25 MOUSE	Q5SX25 mus musculus
21	48	57.8	373	Q6WN23 EUKA	Q6WN23 trichomitus
22	48	57.8	380	Q6WN20 EUKA	Q6WN20 monoceromo
23	48	57.8	380	Q6WN21 EUKA	Q6WN21 monoceromo
24	48	57.8	380	Q6WN22 EUKA	Q6WN22 trichomitus
25	48	57.8	380	Q6WN24 TFIPO	Q6WN24 tritrichomo
26	48	57.8	380	Q6WN28 EUKA	Q6WN28 tetratricho
27	48	57.8	380	Q6WN29 EUKA	Q6WN29 tetratricho
28	48	57.8	380	Q6WP00 EUKA	Q6WP00 tetratricho
29	48	57.8	380	Q6WP01 EUKA	Q6WP01 hypotrichom
30	48	57.8	380	Q6WP02 EUKA	Q6WP02 hypotrichom
31	48	57.8	380	Q6WP03 EUKA	Q6WP03 hypotrichom

32	48	57.8	387	2	Q86ZX6_9FUNG	Q86zx6 karlingiomy
33	48	57.8	398	2	Q8CB15 MOUSE	Q8cb15 mus musculu
34	48	57.8	1192	2	Q5ZKU4_CHICK	Q5zku4 gallus gall
35	48	57.8	1198	2	Q80UK8_MOUSE	Q80uk8 mus musculu
36	48	57.8	1198	2	Q6PCY7_MOUSE	Q6pcy7 mus musculu
37	48	57.8	1202	2	Q6ZPU6_MOUSE	Q6zpu6 mus musculu
38	48	57.8	1204	2	Q9H0H0_HUMAN	Q9h0h0 homo sapien
39	48	57.8	1209	2	Q9ULD3_HUMAN	Q9uld3 homo sapien
40	47	56.6	309	2	Q74CW5_GEOSL	Q74cw5 geobacter s
41	47	56.6	383	1	Y793_METTH	Q26884 methanobact
42	47	56.6	552	2	Q4SIA2_TETNG	Q4sia2 tetraodon n
43	47	56.6	829	2	Q7QA69_ANOGA	Q7qa69 anopheles g
44	47	56.6	1175	2	Q6NS25_XENLA	Q6ns25 xenopus lae
45	47	56.6	1180	2	Q501R5_XENTR	Q501r5 xenopus tro
46	47	56.6	1254	2	Q8IRT7_DROME	Q8irt7 drosophila
47	47	56.6	1266	2	Q9W4O4_DROME	Q9w4o4 drosophila
48	47	56.6	2126	2	Q7PUB0_ANOGA	Q7pub0 anopheles g
49	46.5	56.0	343	2	Q5TQE7_ANOGA	Q5tqe7 anopheles g
50	46	55.4	139	2	Q8X188_PAXIN	Q8x188 paxillus in
51	46	55.4	398	2	Q76HZ6_9METZ	Q76hz6 dicyema sp.
52	46	55.4	445	1	TBB_SCHPO	Q8jlir4 schizosacch
53	46	55.4	448	1	TBB_SCHPO	P05219 suillus bov
54	46	55.4	452	2	Q5SMJ4_CRYNE	Q5smj4 cryptococcu
55	46	55.4	452	2	Q5K876_CRYNE	Q5k876 cryptococcu
56	46	55.4	456	2	Q66668_9GAMA	Q66668 equid herpe
57	46	55.4	477	2	Q6IEH9_FUGRU	Q6ieh9 fugu rubrip
58	46	55.4	1535	2	Q6K9S9_ORYSA	Q6k9s9 oryza sativ
59	45	54.2	99	2	Q6WQ24_BRARE	Q6wq24 brachydanio
60	45	54.2	138	2	Q6ZIR5_ORYSA	Q6zir5 oryza sativ
61	45	54.2	152	2	Q27117_TRIVA	Q27117 trichomonas
62	45	54.2	152	2	Q27118_TRIVA	Q27118 trichomonas
63	45	54.2	152	2	Q69MS6_ORYSA	Q69ms6 oryza sativ
64	45	54.2	211	2	Q67UK6_ORYSA	Q67uk6 oryza sativ
65	45	54.2	289	2	Q533X3_ORENI	Q533x3 oreochromis
66	45	54.2	291	2	Q4P3J3_USTMA	Q4p3j3 ustilago ma
67	45	54.2	341	2	Q726K6_DESVH	Q726k6 desulfovibr
68	45	54.2	365	2	Q84R44_ORYSA	Q84r44 oryza sativ
69	45	54.2	380	2	Q6WNY9_9EUKA	Q6wny9 hexamita in
70	45	54.2	388	2	Q86ZX2_2FUNG	Q86zx2 nowakowekie
71	45	54.2	395	2	Q25165_SPIBA	Q25165 spironucleu
72	45	54.2	415	2	Q8AYD9_MORSA	Q8ayd9 morone saxa
73	45	54.2	426	2	Q20823_CABEL	Q20823 caenorhabdi
74	45	54.2	444	2	Q76DW0_9EUKA	Q76dw0 trichonymph
75	45	54.2	444	2	Q76DW1_9EUKA	Q76dw1 trichonymph
76	45	54.2	445	2	Q7TQO9_XENLA	Q7tqo9 xenopus lae
77	45	54.2	446	1	TBB6_CHICK	P09207 gallus gall
78	45	54.2	446	2	Q27116_TRIVA	Q27116 trichomonas
79	45	54.2	450	1	TBB_BOMMO	P41385 bombyx mori
80	45	54.2	460	2	Q4RVA6_TETNG	Q4rva6 tetraodon n
81	45	54.2	693	2	Q5A586_CANAL	Q5a586 candida alb
82	45	54.2	962	2	Q9ZOM1_ARATH	Q9zom1 arabidopsis
83	44.5	53.6	364	2	Q6ZHF2_ORYSA	Q6zhf2 oryza sativ
84	44	53.0	91	2	Q6W9J4_FUGRU	Q6w9j4 fugu rubrip
85	44	53.0	162	2	Q9AV00_ORYSA	Q9av00 oryza sativ
86	44	53.0	196	2	Q9SJA6_ARATH	Q9sj6 arabidopsis
87	44	53.0	201	2	Q53N79_ORYSA	Q53n79 oryza sativ
88	44	53.0	228	2	Q6ND70_RHOPA	Q6nd70 rhodopseudo
89	44	53.0	267	1	CUTC_XYLFA	Q9pdn8 xylella fas
90	44	53.0	305	2	Q49459_ARATH	Q49459 arabidopsis
91	44	53.0	310	1	PIMI_BRARE	Q9yhx5 brachydanio
92	44	53.0	310	2	Q5C8G1_9PEZI	Q5c8g1 valsa cerat
93	44	53.0	310	2	Q6DI52_BRARE	Q6di52 brachydanio
94	44	53.0	310	2	Q7ZVJ5_BRARE	Q7zv55 brachydanio
95	44	53.0	310	2	Q8JFW9_BRARE	Q8jfw9 brachydanio
96	44	53.0	320	2	Q85515_9CAUD	Q85515 mycobacteri
97	44	53.0	350	2	Q67RA0_SYMTM	Q67ra0 symbiotacte
98	44	53.0	357	2	Q6ZDR4_ORYSA	Q6zdr4 oryza sativ
99	44	53.0	371	2	Q60TD0_CAEBR	Q60td0 caenorhabdi
100	44	53.0	396	2	Q6BUW8_DEBHA	Q6buw8 debaryomyce

## ALIGNMENTS

```

RESULT 1
Q91Y90 PERMA
ID Q91Y90_PERMA PRELIMINARY; PRT; 31 AA.
AC Q91Y90;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Parathyroid hormone (Fragment).
GN Name=Pth;
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Sigmodontinae; Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Prince K.L., Dewey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF382953; AAK63072.1; -; Genomic_DNA.
DR HSSP; P01270; 12WB.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrdorm_sub.
DR PANTHER; PTHR10541; Pthyrdorm_sub; 1.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrdorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 31
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 71.1%; Score 59; DB 2; Length 31;
Best Local Similarity 100.0%; Pred.No. 0.051;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 12
Db 13 AVSEIQLMHNLG 24
|||||
|

RESULT 2
Q91Y91 PERPL
ID Q91Y91_PERPL PRELIMINARY; PRT; 31 AA.
AC Q91Y91;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Parathyroid hormone (Fragment).
GN Name=Pth;
OS Peromyscus polionotus (Oldfield mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Sigmodontinae; Peromyscus.
OX NCBI_TaxID=42413;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Prince K.L., Dewey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF382952; AAK63071.1; -; Genomic_DNA.
DR HSSP; P01270; 12WB.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrdorm_sub.
DR PANTHER; PTHR10541; Pthyrdorm_sub; 1.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrdorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 31
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 71.1%; Score 59; DB 2; Length 31;
Best Local Similarity 100.0%; Pred.No. 0.051;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 12
Db 13 AVSEIQLMHNLG 24
|||||
|

RESULT 3
Q90WZ2 RAT
ID Q90WZ2_RAT PRELIMINARY; PRT; 105 AA.
AC Q90WZ2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothalamic parathyroid hormone.
GN Name=PTH-(1-84);
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
RA Nutley M.T., Parimi S.A., Harvey S.;
RT "Sequence analysis of hypothalamic parathyroid hormone messenger
ribonucleic acid.";
RL Endocrinology 136:5600-5607(1995).
DR EMBL; S80127; AAP32220.1; -; mRNA.
DR HSSP; P01270; 12WB.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrdorm_sub.
DR PANTHER; PTHR10541; Pthyrdorm_sub; 1.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrdorm_sub; 1.
DR PROSITE; PS00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
SQ SEQUENCE 105 AA; 11684 MW; 1BEE71B3F1CF5F70 CRC64;

Query Match 71.1%; Score 59; DB 2; Length 105;
Best Local Similarity 100.0%; Pred.No. 0.2;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 12
Db 22 AVSEIQLMHNLG 33
|||||
|

RESULT 4
PTHY RAT
ID PTHY_RAT STANDARD; PRT; 115 AA.
AC P04089; Q63473;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=Pth;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84135846; PubMed=6321505;
RA Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;

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RT "Gene encoding parathyroid hormone. Nucleotide sequence of the rat  
RT gene and deduced amino acid sequence of rat preproparathyroid  
RT hormone.";  
RL J. Biol. Chem. 259:3320-3329 (1984).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=87316938; PubMed=3628009;  
RA Schmölzer H.-J., Gross G., Widera G., Mayer H.;  
RT "Nucleotide sequence of a full-length cDNA clone encoding  
RT preproparathyroid hormone from pig and rat.";  
RL Nucleic Acids Res. 15:6740-6740 (1987).  
RN [3]  
RP NUCLEOTIDE SEQUENCE OF 10-115.  
RC TISSUE=Parathyroid;  
RA Schmölzer H.-J., Gross G., Mayer H.;  
RT "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid  
RT hormone.";  
RL Adv. Gene Technol. 21:228-229 (1984).  
RN [4]  
RP NUCLEOTIDE SEQUENCE OF 32-115.  
RC STRAIN=Sprague-Dawley; TISSUE=Brain, Liver, and Parathyroid;  
RX MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;  
RA Nutley M.T., Paximi S.A., Harvey S.;  
RT "Sequence analysis of hypothalamic parathyroid hormone messenger  
RT ribonucleic acid.";  
RL Endocrinology 136:5600-5607 (1995).  
CC -1- FUNCTION: PTH elevates calcium level by dissolving the salts in  
CC bone and preventing their renal excretion.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Hypothalamus and parathyroid gland.  
CC -1- SIMILARITY: Belongs to the parathyroid hormone family.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC -----  
CC EMBL; K01268; AAA41979.1; -; Genomic DNA.  
CC EMBL; X05721; CAA29192.1; -; mRNA.  
CC EMBL; M54875; AAA57156.1; -; mRNA.  
CC EMBL; S80127; -; NOT\_ANNOTATED\_CDS; mRNA.  
CC PIR; A05091; A05091.  
CC HSP; P01270; 12WB.  
CC Ensembl; ENSRNOG00000014318; Rattus norvegicus.  
CC RGD; 3440; Pth.  
CC InterPro; IPR001415; Parathyroid hrm.  
CC InterPro; IPR003626; PTH related.  
CC InterPro; IPR003625; Pthyrhorm sub.  
CC PANTHER; PTHR10541; Pthyrhorm\_sub; 1.  
CC Pfam; PF01279; Parathyroid; 1.  
CC PIRSF; PIRSF001832; PTH; 1.  
CC ProDom; PD013225; PTH related; 1.  
CC ProDom; PD010687; Pthyrhorm\_sub; 1.  
CC SMART; SM00087; PTH; 1.  
CC PROSITE; PS00335; PARATHYROID; 1.  
CC Hormone; Signal.  
CC SIGNAL 1 25  
CC PROPEP 26 31  
CC CHAIN 32 115  
CC Parathyroid hormone.  
CC C -> Y (in Ref. 3).  
CC A -> T (in Ref. 3).  
CC CONFLICT 23 23  
CC CONFLICT 33 33  
CC CONFLICT 62 62  
CC V -> G (in Ref. 3).  
CC V -> G (in Ref. 3).  
CC SEQUENCE 115 AA; 12722 MW; 7B434CFCAS28B230 CRC64;  
SQ  
Query Match 71.1%; Score 59; DB 1; Length 115;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AVSEIQLMHNILG 12  
Db 32 AVSEIQLMHNILG 43  
|||||

RESULT 5  
Q9Z0L6\_MOUSE  
ID Q9Z0L6\_MOUSE PRELIMINARY; PRT; 115 AA.  
AC Q9Z0L6;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
DE Parathyroid hormone precursor.  
GN Name=Pth;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=129/SV;  
RA Karaplis A.C., He B., Hiou-Tim F.F.T., Al-Akad B., Kronenberg H.M.;  
RT "Cloning of the murine gene encoding parathyroid hormone: genomic  
RT organization and nucleotide sequence.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Thyroid;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Thyroid;  
RG NIH WGC Project;  
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF066075; AAC9956.1; -; Genomic DNA.  
DR EMBL; BC099456; AAH99456.1; -; mRNA.  
DR HSP; P01270; 12WB.  
DR Ensembl; ENSMUSG00000059077; Mus musculus.  
DR MGI; MGI:97799; Pth.  
DR GO; GO:0005615; C:extracellular space; IDA.  
DR GO; GO:0005179; F:hormone activity; IDA.  
DR GO; GO:0006874; P:calcium ion homeostasis; TAS.  
DR InterPro; IPR001415; Parathyroid hrm.  
DR InterPro; IPR003625; Pthyrhorm\_sub.  
DR PANTHER; PTHR10541; Pthyrhorm\_sub; 1.  
DR Pfam; PF01279; Parathyroid; 1.  
DR PIRSF; PIRSF001832; PTH; 1.  
DR ProDom; PD010687; Pthyrhorm\_sub; 1.  
DR SMART; SM00087; PTH; 1.  
DR PROSITE; PS00335; PARATHYROID; 1.  
DR SIGNAL 1 25  
DR PROPEP 26 31  
DR CHAIN 32 115  
DR Parathyroid hormone.  
DR C -> Y (in Ref. 3).  
DR A -> T (in Ref. 3).  
DR CONFLICT 23 23  
DR CONFLICT 33 33  
DR CONFLICT 62 62  
DR V -> G (in Ref. 3).  
DR V -> G (in Ref. 3).  
DR SEQUENCE 115 AA; 12825 MW; DA43FABBCB4E2FD9 CRC64;  
SQ  
Query Match 71.1%; Score 59; DB 1; Length 115;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AVSEIQLMHNILG 12  
Db 32 AVSEIQLMHNILG 43  
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Query Match          71.1%; Score 59; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. NO. 0.22;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 12
DB 32 AVSEIQLMHNLG 43

RESULT 6
QPN1VO HORSE PRELIMINARY; PRT; 86 AA.
AC QPN1VO;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Parathyroid hormone (fragment).
GN Name=PTH;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20082971; PubMed=10613847; DOI=10.1101/gr.9.12.1239;
RA Caetano A.R., Shue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA Bowling A.T., Murray J.D.;
RT "A comparative gene map of the horse (Equus caballus).";
RL Genome Res. 9:1239-1249(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Shue Y.-L., Caetano A.R., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA Murray J.D., Bowling A.T.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF134233; AAR62347.1; -; Genomic_DNA.
DR HSPF; P01270; 1FT1.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001415; Parathyroid_hrm.
DR Inceptro; IPR003625; Pthyhorm_sub.
DR PANTHER; PTHR10541; Pthyhorm_sub; 1.
DR Pfam; PF01279; Parathyroid; 1.
DR Prodom; PD010687; Pthyhorm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1
FT SEQUENCE 86 AA; 9805 MW; 253184EA681A2022 CRC64;

Query Match          67.5%; Score 56; DB 2; Length 86;
Best Local Similarity 91.7%; Pred. NO. 0.48;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 12
DB 3 SVSEIQLMHNLG 14

RESULT 7
PTHY HUMAN
ID PTHY HUMAN STANDARD; PRT; 115 AA.
AC P01270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).
GN Name=PTH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RX MEDLINE=82150870; PubMed=6950381;
RA Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;
RT "Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.";
RN Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83169834; PubMed=6220408;
RA Vasicek T.J., McCavitt B.E., Freeman M.W., Fennick B.J., Hendy G.N.,
RA Potts J.T. Jr., Rich A., Kronenberg H.M.;
RT "Nucleotide sequence of the human parathyroid hormone gene.";
RN Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).
RN [3]
RP PROTEIN SEQUENCE OF 26-37.
RX MEDLINE=74174967; PubMed=4933516;
RA Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;
RT "Structural analysis of human parathyroid hormone by a new microsequencing approach.";
RN Nature 249:155-157(1974).
RN [4]
RP PROTEIN SEQUENCE OF 26-40.
RX PubMed=15340161; DOI=10.1110/p9.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally verified cleavage sites.";
RN Protein Sci. 13:2819-2824(2004).
RN [5]
RP PROTEIN SEQUENCE OF 32-68.
RX MEDLINE=74111656; PubMed=4521809;
RA Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,
RA O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;
RT "The amino-acid sequence of the amino-terminal 37 residues of human parathyroid hormone.";
RN Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).
RN [6]
RP PROTEIN SEQUENCE OF 61-83 AND 84-115.
RX MEDLINE=79082855; PubMed=728431;
RA Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,
RA Potts J.T. Jr.;
RT "Complete amino acid sequence of human parathyroid hormone.";
RN Biochemistry 17:5723-5729(1978).
RN [7]
RP PROTEIN SEQUENCE OF 75-100.
RA Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,
RA O'Riordan J.L.H., Potts J.T. Jr.;
RT (In) Talmadge R.V., Owen M., Parsons J.A. (eds.);
RL Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation, Amsterdam (1975).
RN [8]
RP SEQUENCE REVISION.
RX MEDLINE=75146516; PubMed=1125201;
RA Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;
RT "A reinvestigation of the amino-terminal sequence of human parathyroid hormone.";
RN Biochemistry 14:1842-1847(1975).
RN [9]
RP SYNTHESIS OF 32-65.
RX MEDLINE=75059220; PubMed=4474131;
RA Tregear G.W., van Rietschoten J., Green E., Niall H.D., Keutmann H.T.,
RA Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;
RT "Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of human parathyroid hormone.";
RN Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
RN [10]
RP SYNTHESIS OF 32-65.
RX MEDLINE=7327467; PubMed=4721748;
RA Andreotta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,
RA Riniker B., Rittel W., Sieber F.;
RT "Synthesis of sequence 1-34 of human parathyroid hormone.";
RN Helv. Chim. Acta 56:470-473(1973).
RN [11]
RP STRUCTURE BY NMR OF 32-65.
RX MEDLINE=91299748; PubMed=2069952;

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RA Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;  
 RT "Investigation of the solution structure of the human parathyroid  
 RT hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry, and  
 RT molecular dynamics calculations."; Biochemistry 30:6936-6942(1991).  
 RL [12]  
 RN STRUCTURE BY NMR OF 32-65.  
 RP MEDLINE=93345518; PubMed=8344299;  
 RX Barden J.A., Cuthbertson R.M.;  
 RA "Stabilized NMR structure of human parathyroid hormone (1-34).";  
 RL Eur. J. Biochem. 215:315-321(1993).  
 RN [13]  
 RP STRUCTURE BY NMR OF 32-68.  
 RX MEDLINE=95318084; PubMed=7797503; DOI=10.1074/jbc.270.25.15194;  
 RA Marx U.C., Austermann S., Beyer P., Adermann W.-G., Rosch P.;  
 RA Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,  
 RA Roesch P.;  
 RT "Structure of human parathyroid hormone 1-37 in solution."; J. Biol. Chem. 270:15194-15202(1995).  
 RL [14]  
 RN STRUCTURE BY NMR OF 32-70.  
 RP MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;  
 RX Marx U.C., Adermann K., Beyer P., Forssmann W.-G., Rosch P.;  
 RA "Solution structures of human parathyroid hormone fragments hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment bpTH(1-37)."; Biochem. Biophys. Res. Commun. 267:213-220(2000).  
 RL [15]  
 RN VARIANT FTH ARG-18.  
 RP MEDLINE=91009811; PubMed=2212001;  
 RX Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A., Kronenberg H.M.;  
 RA "Mutation of the signal peptide-encoding region of the preproparathyroid hormone gene in familial isolated hypoparathyroidism."; J. Clin. Invest. 86:1084-1087(1990).  
 RL [16]  
 RN VARIANT FTH PRO-23.  
 RP PubMed=10523031;  
 RX Sunthorncheparakul T., Churesigaw S., Ngowngarmratana S.;  
 RA "A novel mutation of the signal peptide of the preproparathyroid hormone gene associated with autosomal recessive familial isolated hypoparathyroidism."; J. Clin. Endocrinol. Metab. 84:3792-3796(1999).  
 RL [17]  
 RN FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.  
 CC [18]  
 CC DISEASE: Defects in PTH are a cause of familial isolated hypoparathyroidism (FIH) [MIM:146200]. FIH exist both as autosomal dominant and recessive forms of hypoparathyroidism.  
 CC [19]  
 CC SIMILARITY: Belongs to the parathyroid hormone family.  
 CC  
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 CC  
 CC EMBL: J00301; AAA60215.1; -; Genomic DNA.  
 CC EMBL: V00597; CAA23843.1; -; mRNA.  
 CC EMBL: A29146; CAA01956.1; -; Unassigned DNA.  
 CC PIR: A19339; PTHU.  
 CC PDB: 1BWK; NMR; @=32-70.  
 CC PDB: 1ET1; X-ray; A/B=32-65.  
 CC PDB: 1ET2; Model; A=32-65.  
 CC PDB: 1FVY; NMR; A=32-62.  
 CC PDB: 1HPH; NMR; @=32-68.  
 CC PDB: 1HPY; NMR; @=32-65.  
 CC PDB: 1HTH; NMR; @=32-65.  
 CC PDB: 1ZWA; NMR; @=32-65.  
 CC PDB: 1ZWB; NMR; @=33-68.  
 CC PDB: 1ZWD; NMR; @=34-68.  
 CC PDB: 1ZWE; NMR; @=35-68.  
 CC PDB: 1ZWF; NMR; @=35-68.

PDB; 1ZWG; NMR; @=-.  
 DR Ensembl: ENSG00000152266; Homo sapiens.  
 DR HGNC: HGNC:9606; PTH.  
 DR MIM; 168450; -.  
 DR MIM; 146200; -.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0005179; F:hormone activity; TAS.  
 DR GO; GO:0045453; F:bone resorption; NAS.  
 DR GO; GO:0006874; P:calcium ion homeostasis; NAS.  
 DR GO; GO:0046058; P:cAMP metabolism; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.  
 DR GO; GO:0008628; P:induction of apoptosis by hormones; TAS.  
 DR GO; GO:0001501; P:skeletal development; TAS.  
 DR InterPro: IPR001415; Parathyrd hrm.  
 DR InterPro: IPR003625; Pthyrdorm\_sub.  
 DR PANTHER: PTHR10541; Pthyrdorm\_sub; 1.  
 DR Pfam: PF01279; Parathyroid; 1.  
 DR PIRSF: PIRSF001832; PTH; 1.  
 DR ProDom: PD010687; Pthyrdorm\_sub; 1.  
 DR SMART: SM00087; PTH; 1.  
 DR PROSITE: PS00335; PARATHYROID; 1.  
 KW 3D-structure; Direct protein sequencing; Disease mutation; Hormone;  
 KW Signal.  
 FT SIGNAL 1 25  
 FT PROPEP 26 31  
 FT CHAIN 32 115  
 FT VARIANT 18 18  
 FT  
 FT VARIANT 23 23  
 FT  
 FT CONFLICT 107 107  
 FT HELIX 34 64  
 FT SEQUENCE 115 AA; 12861 MW; 849015736AE5597 CRC64;  
 SQ  
 Query Match 67.5%; Score 56; DB 1; Length 115;  
 Best Local Similarity 91.7%; Pred. No. 0.67;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AVSEIQLMHNLG 12  
 :|||||  
 DB 32 SVSEIQLMHNLG 43  
 RESULT 8  
 ID PTH MACFA STANDARD; PRT; 115 AA.  
 AC Q9XT35;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Parathyroid hormone precursor (Parathyrin) (PTH).  
 GN Name=PTH;  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopithecoidea; Cercopithecinae; Macaca.  
 OC NCBI\_TaxID=9541;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Malaivijitnond S., Takenaka O.;  
 RT "Nucleotide sequences of parathyroid gene in five species of macaque of Thailand."; J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).  
 RL J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).  
 CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the parathyroid hormone family.  
 CC  
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF130257; AAD42777.1; -; Genomic_DNA.
CC DR HSSP; P01270; 1BT1.
CC DR InterPro; IPR001415; Parathyroid_hrm.
CC DR InterPro; IPR003625; Pthyrrhorm_sub.
CC DR PANTHER; PTHR10541; Pthyrrhorm_sub; 1.
CC DR Pfam; PF01279; Parathyroid; 1.
CC DR PIRSF; PIRSF001832; PTH; 1.
CC DR PRODOM; PD010687; Pthyrrhorm_sub; 1.
CC DR SMART; SM00087; PTH; 1.
CC DR PROSITE; PS00335; PARATHYROID; 1.
CC KW Hormone; Signal.
CC FT SIGNAL 1 25 By similarity.
CC FT PROPEP 26 31
CC FT CHAIN 32 115 Parathyroid hormone.
CC SQ SEQUENCE 115 AA; 12890 MW; 8C2500EF24BE597 CRC64;

Query Match 67.5%; Score 56; DB 1; Length 115;
Best Local Similarity 91.7%; Pred. No. 0.67;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMNLG 12
DB :|||||
32 SVSEIQLMNLG 43

RESULT 9
PTHY_PIG
ID PTHY_PIG STANDARD; PRT; 115 AA.
AC P01269;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1998 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=PTH;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sub;
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87316938; PubMed=3628009;
RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT "Nucleotide sequence of a full-length cDNA clone encoding
RT preproparathyroid hormone from pig and rat.";
RL Nucleic Acids Res. 15:6740-6740(1987).
RN [2]
RP PROTEIN SEQUENCE OF 26-115.
RX MEDLINE=76018954; PubMed=1164500;
RA Chu L.L.H., Huang W.-Y., Littlelike E.T., Hamilton J.W., Cohn D.V.;
RT "Porcine preproparathyroid hormone. Identification, biosynthesis, and
RT partial amino acid sequence.";
RL Biochemistry 14:3631-3635(1975).
RN [3]
RP PROTEIN SEQUENCE OF 32-115.
RX MEDLINE=74253117; PubMed=4840833;
RA Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
RA Potts J.T., Jr.
RT "The amino acid sequence of porcine parathyroid hormone.";
CC -!- FUNCTION. PTH elevates calcium level by dissolving the salts in
CC -!- bones and preventing their renal excretion.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC -----
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CC use as long as its content is in no way modified and this statement is not

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CC removed.
CC -----
CC EMBL; X05722; CAA29193.1; -; mRNA.
CC DR PIR; B26806; PTPG.
CC DR HSSP; P01270; 1BMX.
CC DR InterPro; IPR001415; Parathyroid_hrm.
CC DR InterPro; IPR003625; Pthyrrhorm_sub.
CC DR PANTHER; PTHR10541; Pthyrrhorm_sub; 1.
CC DR Pfam; PF01279; Parathyroid; 1.
CC DR PIRSF; PIRSF001832; PTH; 1.
CC DR PRODOM; PD010687; Pthyrrhorm_sub; 1.
CC DR SMART; SM00087; PTH; 1.
CC DR PROSITE; PS00335; PARATHYROID; 1.
CC KW Direct protein sequencing; Hormone; Signal.
CC FT SIGNAL 1 25
CC FT PROPEP 26 31
CC FT CHAIN 32 115 Parathyroid hormone.
CC SQ SEQUENCE 115 AA; 12852 MW; 9FE8BCDE614EAC16 CRC64;

Query Match 67.5%; Score 56; DB 1; Length 115;
Best Local Similarity 91.7%; Pred. No. 0.67;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMNLG 12
DB :|||||
32 SVSEIQLMNLG 43

RESULT 10
Q4VB48 HUMAN
ID Q4VB48 HUMAN PRELIMINARY; PRT; 115 AA.
AC Q4VB48;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Parathyroid hormone, preproprotein.
GN Name=PTH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo;
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=PCR rescued clones; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U.,
RA Smerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=PCR rescued clones;
CC NIH MGC project;
CC Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC EMBL; BC096143; AAH96143.1; -; mRNA.
CC EMBL; BC096144; AAH96144.1; -; mRNA.

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DR EMBL: BC096145; AAH96145.1; -; mRNA.
DR EMBL: BC096142; AAH96142.1; -; mRNA.
DR InterPro: IPR001415; Parathyroid_hrm.
DR Pfam: PF01279; Parathyroid; 1.
DR PIRSF: PIRSF001832; PTH; 1.
DR ProDom: PD010687; Pthyrhorm_sub; 1.
DR SMART: SM00087; PTH; 1.
DR PROSITE: PS00335; PARATHYROID; 1.
SQ SEQUENCE 115 AA; 12861 MW; 849015736AE5597 CRC64;

Query Match 67.5%; Score 56; DB 2; Length 115;
Best Local Similarity 91.7%; Pred. No. 0.67;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db :|||||
32 SVSEIQLMHNLG 43

RESULT 11
Q5TLZ1 BRARE PRELIMINARY; PRT; 102 AA.
AC Q5TLZ1;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Parathyroid hormone.
GN Name=pth1; Synonym=PTH;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP Okabe M., Graham A.;
RT "The origin of the parathyroid gland.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:17716-17719(2004).
DR EMBL: AB175679; BAD72832.1; -; mRNA.
DR ZFIN: ZDB-GENE-040623-1; pth1.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005179; F:hormone activity; IEA.
DR InterPro: IPR001415; Parathyroid_hrm.
DR PANTHER: PTHR10541; Pthyrhorm_sub; 1.
DR Pfam: PF01279; Parathyroid; 1.
DR ProDom: PD010687; Pthyrhorm_sub; 1.
DR SMART: SM00087; PTH; 1.
SQ SEQUENCE 102 AA; 11641 MW; 5AA7B0F8A4110764 CRC64;

Query Match 66.3%; Score 55; DB 2; Length 102;
Best Local Similarity 83.3%; Pred. No. 0.84;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db :|||||
36 AVNEVQLMHNLG 47

RESULT 12
Q6WQ25 BRARE PRELIMINARY; PRT; 102 AA.
AC Q6WQ25;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Parathyroid hormone ligand type-1.
GN Name=pth1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.

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OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14684608; DOI=10.1210/en.2003-0964;
RA Gensure R.C., Ponugoti B., Gunee Y., Papasani M.R., Lamske B.,
RA Bastepe M., Rubin D.A., Juppner H.;
RT "Identification and characterization of two parathyroid hormone-like
RT molecules in zebrafish.";
RL Endocrinology 145:1634-1639(2004).
DR EMBL: AY275669; AAQ16566.1; -; mRNA.
DR ZFIN: ZDB-GENE-040623-1; pth1.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005179; F:hormone activity; IEA.
DR InterPro: IPR001415; Parathyroid_hrm.
DR InterPro: IPR003625; Pthyrhorm_sub.
DR PANTHER: PTHR10541; Pthyrhorm_sub; 1.
DR Pfam: PF01279; Parathyroid; 1.
DR ProDom: PD010687; Pthyrhorm_sub; 1.
DR SMART: SM00087; PTH; 1.
SQ SEQUENCE 102 AA; 11690 MW; 5AA7A84FF4110764 CRC64;

Query Match 66.3%; Score 55; DB 2; Length 102;
Best Local Similarity 83.3%; Pred. No. 0.84;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db :|||||
36 AVNEVQLMHNLG 47

RESULT 13
PTHY_BOVIN STANDARD; PRT; 115 AA.
AC P01286;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=PTH;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=80056617; PubMed=388425;
RA Kronenberg H.M., McDavitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
RA Potts J.T. Jr., Rich A.;
RT "Cloning and nucleotide sequence of DNA coding for bovine
RT preproparathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82037785; PubMed=6170060;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Introduction by molecular cloning of artifactual inverted sequences
RT at the 5' terminus of the sense strand of bovine parathyroid hormone
RT cDNA.";
RN [3]
RP Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83105964; PubMed=6185374; DOI=10.1016/0303-7207(82)90136-8;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
RL Mol. Cell. Endocrinol. 28:411-424(1982).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84282483; PubMed=6086460; DOI=10.1016/0378-1119(84)90149-5;
RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
RT "Isolation and complete nucleotide sequence of the gene for bovine
RT parathyroid hormone.";
RL Gene 28:319-329(1984).

```

[5]  
RP PROTEIN SEQUENCE OF 26-115.  
RX MEDLINE=74142666; PubMed=4522780;  
RA Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,  
BA Cohn D.V.;  
RT "The N-terminal amino-acid sequence of bovine parathyroid  
hormone."; Proc. Natl. Acad. Sci. U.S.A. 71:653-656 (1974).  
[6]  
RP PROTEIN SEQUENCE OF 32-115.  
RX MEDLINE=71076162; PubMed=5531031;  
RA Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,  
RA Aurbach G.D., Potts J.T. Jr.  
RT "The amino acid sequence of bovine parathyroid hormone I.";  
[7]  
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588 (1970).  
[8]  
RP PROTEIN SEQUENCE OF 32-115.  
RX MEDLINE=71063634; PubMed=5275384;  
RA Brewer H.B. Jr., Ronan R.;  
RT "Bovine parathyroid hormone: amino acid sequence.";  
[9]  
RL Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869 (1970).  
[10]  
RP SYNTHESIS OF 32-65.  
RX MEDLINE=71091588; PubMed=4322265;  
RA Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,  
RA Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;  
RT "Synthesis of a biologically active N-terminal tetrapeptide  
of parathyroid hormone."; Proc. Natl. Acad. Sci. U.S.A. 68:63-67 (1971).  
[11]  
RP STRUCTURE BY NMR OF 32-68.  
RX MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;  
RA Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;  
RT "Solution structures of human parathyroid hormone fragments hPTH(1-34)  
and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";  
[12]  
RL Biochem. Biophys. Res. Commun. 267:213-220 (2000).  
[13]  
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in  
bone and preventing their renal excretion.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
DR EMBL; V00106; CAA23439.1; -; mRNA.  
DR EMBL; J00024; AAA30747.1; -; mRNA.  
DR EMBL; K01938; AAA30749.1; -; Genomic DNA.  
DR EMBL; M25082; AAA30748.1; -; mRNA.  
DR PIR; A24949; PTBO.  
DR PDB; 1ZWC; NMR; @=32-68.  
DR InterPro; IPR001415; Parathyrd\_hrm.  
DR InterPro; IPR003625; Pthythorm\_sub.  
DR PANTHER; PTHR10541; Pthythorm\_sub; 1.  
DR Pfam; PF01279; Parathyroid; 1.  
DR PIRSF; PIRSF001832; PTH; 1.  
DR ProDom; PD010687; Pthythorm\_sub; 1.  
DR SMART; SM00087; PTH; 1.  
DR PROSITE; PS00335; PARATHYROID; 1.  
KW 3D-structure; Direct protein sequencing; Hormone; Signal.  
FT SIGNAL 1 25  
FT PROPEP 26 31 Parathyroid hormone.  
FT CHAIN 106 106 V -> G (in Ref. 4).  
FT CONFLICT 37 40  
FT HELIX 41 42  
FT TURN 51 52  
FT TURN 53 60  
FT HELIX 61 63  
SQ SEQUENCE 115 AA; 12980 MW; 2ED246B348880710 CRC64;

Query Match 66.3%; Score 55; DB 1; Length 115;  
Best Local Similarity 91.7%; Pred. No. 0.96;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 1 AVSEIQMHNLG 12  
Db 32 AVSEIQMHNLG 43  
RESULT 14  
ID\_PTHY\_CHICK STANDARD; PRT; 119 AA.  
AC P15743;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Parathyroid hormone precursor (PTH).  
GN Name=PTH (Chicken).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Aukosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
[1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=89219100; PubMed=2710135;  
RA Russell J., Sherwood L.M.;  
RT "Nucleotide sequence of the DNA complementary to avian (chicken)  
preparathyroid hormone mRNA and the deduced sequence of the hormone  
precursor."; Mol. Endocrinol. 3:325-331 (1989).  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=89284968; PubMed=3251402;  
RA Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,  
RA Kronenberg H.M.;  
RT "Nucleotide sequence of cloned cDNAs encoding chicken  
preparathyroid hormone."; J. Bone Miner. Res. 3:689-698 (1988).  
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in  
bone and preventing their renal excretion.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
DR EMBL; M31604; AAA49093.1; -; mRNA.  
DR EMBL; M36522; AAB02866.1; -; mRNA.  
DR PIR; A34937; A34937.  
DR HSRF; P01270; IFVT.  
DR EMBL; ENSGALG00000005358; Gallus gallus.  
DR InterPro; IPR001415; Parathyrd\_hrm.  
DR InterPro; IPR003625; Pthythorm\_sub.  
DR PANTHER; PTHR10541; Pthythorm\_sub; 1.  
DR Pfam; PF01279; Parathyroid; 1.  
DR PIRSF; PIRSF001832; PTH; 1.  
DR ProDom; PD013225; PTH\_related; 1.  
DR ProDom; PD010687; Pthythorm\_sub; 1.  
DR SMART; SM00087; PTH; 1.  
DR PROSITE; PS00335; PARATHYROID; 1.  
KW Hormone; Signal.  
FT SIGNAL 1 25  
FT PROPEP 26 31 Parathyroid hormone.  
FT CHAIN 32 119  
SQ SEQUENCE 119 AA; 13943 MW; B309D8E772997F6E CRC64;  
Query Match 63.9%; Score 53; DB 1; Length 119;  
Best Local Similarity 83.3%; Pred. No. 2.1;

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Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNIG 12
Db 32 SVSEIQLMHNIG 43

RESULT 15
PTHY_CANFA STANDARD; PRT; 115 AA.
AC P52212;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=PTH;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Parathyroid;
RX MEDLINE=9536966; PubMed=7642102; DOI=10.1016/0378-1119(94)00912-C;
RA Rosol T.J., Steinmeyer C.L., McCauley L.K., Greene A., Dewille J.W.,
RA Capen C.C.;
RT "Sequences of the cDNAs encoding canine parathyroid hormone-related
RT protein and parathyroid hormone.";
RL Gene 160:241-243(1995).
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC bone and preventing their renal excretion.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U15662; AAA82584.1; -; mRNA.
CC PIR; JC4202; JC4202.
CC HSP; P01268; IZWC.
CC Ensembl; ENSCAG00000008177; Canis familiaris.
CC InterPro; IPR001415; Parathyrd_hrm.
CC InterPro; IPR003625; Pthyrdorm_sub.
CC PANTHER; PTHR10541; pthyrdorm_sub; 1.
CC Pfam; PF01279; Parathyroid; 1.
CC PIRSF; PIRSF001832; PTH; 1.
CC ProDom; PD010687; Pthyrdorm_sub; 1.
CC SMART; SMO0087; PTH; 1.
CC PROSITE; PS00335; PARATHYROID; 1.
CC Hormone; Signal.
CC SIGNAL 1 25 By similarity.
CC PROPEP 26 31 By similarity.
CC CHAIN 32 115 Parathyroid hormone.
CC SEQUENCE 115 AA; 12957 MW; FC38F77F1C8CFE56 CRC64;

Query Match 62.7%; Score 52; DB 1; Length 115;
Best Local Similarity 83.3%; Pred. No. 2.8;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNIG 12
Db 32 SVSEIQLMHNIG 43

RESULT 16
PTHY_FELCA STANDARD; PRT; 115 AA.
AC Q9GL67;
DT 05-JUL-2004 (Rel. 44, Created)
ID -PTHY_FELCA
OX O9GL67;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Scherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natile A.G., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozlyavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";

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05-JUL-2004 (Rel. 44, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=PTH;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;
RT "Molecular cloning of feline preproparathyroid hormone.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC bone and preventing their renal excretion (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF309967; AAG30545.1; -; mRNA.
CC HSP; P01268; IZWC.
CC InterPro; IPR001415; Parathyrd_hrm.
CC InterPro; IPR003625; Pthyrdorm_sub.
CC PANTHER; PTHR10541; Pthyrdorm_sub; 1.
CC Pfam; PF01279; Parathyroid; 1.
CC PIRSF; PIRSF001832; PTH; 1.
CC ProDom; PD010687; Pthyrdorm_sub; 1.
CC SMART; SMO0087; PTH; 1.
CC PROSITE; PS00335; PARATHYROID; 1.
CC Hormone; Signal.
CC SIGNAL 1 25 By similarity.
CC PROPEP 26 31 By similarity.
CC CHAIN 32 115 Parathyroid hormone.
CC SEQUENCE 115 AA; 12921 MW; 80CD557CC6A1A47E CRC64;

Query Match 62.7%; Score 52; DB 1; Length 115;
Best Local Similarity 83.3%; Pred. No. 2.8;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNIG 12
Db 32 SVSEIQLMHNIG 43

RESULT 17
Q8TVLI_METKA
ID Q8TVLI_METKA PRELIMINARY; PRT; 394 AA.
AC Q8TVLI;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acetyl-CoA acetyltransferase.
GN OrderedLocustNames=MK1378;
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Scherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natile A.G., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozlyavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";

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RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR EMBL; AE010431; AM02591.1; -, Genomic DNA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR002155; Thiolase.
DR Pfam; PF02803; Thiolase_C; 1.
DR Dfam; DF00108; Thiolase_N; 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 394 AA; 42063 MW; A816CFFPFDE634E4 CRC64;

Query Match 60.2%; Score 50; DB 2; Length 394;
Best Local Similarity 64.3%; Pred. No. 23;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 SEIQLMHNLGGGG 16
Db :|||:|||||
370 AEIGLTHNVGSGG 383

RESULT 19
Q5SGS9 D1CDI
ID Q5SGS9_D1CDI PRELIMINARY; PRT; 885 AA.
AC Q5SGS9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=BD0189350;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachébat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Mader A., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Harper D., Lindsey R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulsegged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Bartell B., Kuspa A.,
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0(2005).
CC -!- CAUTION: the sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
DR EMBL; AAF101000009; EAL73219.1; -, Genomic DNA.
SQ SEQUENCE 885 AA; 97636 MW; 7F56E9DFBC85BEEA CRC64;

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Query Match 59.0%; Score 49; DB 2; Length 885;
Best Local Similarity 55.0%; Pred. No. 84;
Matches 11; Conservative 2; Mismatches 1; Indels 6; Gaps 1;

QY 3 SEIQLMH-----NLGGGG 16
Db :|||:|||||
157 SPIQLIHNLDSNVGGGG 176

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RESULT 19
Q5SXZ6 MOUSE
ID Q5SXZ6_MOUSE PRELIMINARY; PRT; 140 AA.
AC Q5SXZ6;

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DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel protein (Fragment).
GN Name=OTTMUSP0000001188; ORFNames=RP23-50E4.2-005;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Phillimore B.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL592065; CAI25864.1; -, Genomic DNA.
FT NON TER 140
SQ SEQUENCE 140 AA; 15387 MW; F5108D76C2FFD8EE CRC64;

Query Match 57.8%; Score 48; DB 2; Length 140;
Best Local Similarity 62.5%; Pred. No. 15;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLGGGG 16
Db :|||:|||||
92 ASKEQQLRHKLGGSG 107

RESULT 20
Q5SXZ5 MOUSE
ID Q5SXZ5_MOUSE PRELIMINARY; PRT; 190 AA.
AC Q5SXZ5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel protein (Fragment).
GN Name=OTTMUSP0000001189; ORFNames=RP23-50E4.2-007;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Phillimore B.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL592065; CAI25865.1; -, Genomic DNA.
FT NON TER 190
SQ SEQUENCE 190 AA; 20892 MW; F0DC4B41A26B53C5 CRC64;

Query Match 57.8%; Score 48; DB 2; Length 190;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLGGGG 16
Db :|||:|||||
92 ASKEQQLRHKLGGSG 107

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Search completed: November 21, 2005, 16:42:55
Job time : 238 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 16:38:20 : Search time 46 Seconds  
(without alignments)  
28.757 Million cell updates/sec

Title: SEQ-NEW

Perfect score: 83

Sequence: 1 avseiqmhnlgggg 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep:\*
  - 2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep:\*
  - 3: /cgn2\_6/ptodata/1/iaa/H-COMB.pep:\*
  - 4: /cgn2\_6/ptodata/1/iaa/PCTUS-COMB.pep:\*
  - 5: /cgn2\_6/ptodata/1/iaa/RE-COMB.pep:\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	59	71.1	12	2	US-09-730-174A-5
2	59	71.1	14	2	US-09-421-379-5
3	59	71.1	15	2	US-09-730-174A-11
4	59	71.1	27	2	US-09-448-867-5
5	59	71.1	27	2	US-09-448-867-9
6	59	71.1	27	2	US-09-447-800-7
7	59	71.1	27	2	US-10-157-076-5
8	59	71.1	27	2	US-10-157-076-9
9	59	71.1	28	2	US-09-448-867-4
10	59	71.1	28	2	US-09-448-867-8
11	59	71.1	28	2	US-10-157-076-4
12	59	71.1	28	2	US-10-157-076-8
13	59	71.1	30	2	US-09-843-221A-48
14	59	71.1	31	2	US-09-228-990-31
15	59	71.1	33	2	US-09-447-800-6
16	59	71.1	34	1	US-08-488-105-3
17	59	71.1	34	1	US-08-488-105-9
18	59	71.1	34	1	US-08-488-105-15
19	59	71.1	34	2	US-09-447-800-5
20	59	71.1	34	2	US-09-843-221A-25
21	59	71.1	34	2	US-09-623-548A-274
22	59	71.1	34	2	US-10-340-484-22
23	59	71.1	34	2	US-10-340-484-23
24	59	71.1	34	2	US-09-657-276-274
25	59	71.1	35	1	US-08-142-551B-52
26	59	71.1	84	2	US-09-843-221A-11
27	57	68.7	31	2	US-09-228-990-32

28	57	68.7	35	1	US-08-142-551B-56	Sequence 56, Appl
29	56	67.5	12	2	US-09-730-174A-3	Sequence 3, Appl
30	56	67.5	13	1	US-08-411-726-3	Sequence 3, Appl
31	56	67.5	14	2	US-09-421-379-3	Sequence 3, Appl
32	56	67.5	15	2	US-09-730-174A-9	Sequence 9, Appl
33	56	67.5	27	2	US-09-448-867-7	Sequence 7, Appl
34	56	67.5	27	2	US-09-448-867-13	Sequence 13, Appl
35	56	67.5	27	2	US-09-447-800-10	Sequence 10, Appl
36	56	67.5	27	2	US-10-157-076-7	Sequence 7, Appl
37	56	67.5	27	2	US-10-157-076-13	Sequence 13, Appl
38	56	67.5	28	2	US-09-406-813-3	Sequence 3, Appl
39	56	67.5	28	2	US-09-406-813-6	Sequence 6, Appl
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41	56	67.5	28	2	US-09-448-867-12	Sequence 12, Appl
42	56	67.5	28	2	US-09-843-221A-52	Sequence 52, Appl
43	56	67.5	28	2	US-09-843-221A-168	Sequence 168, App
44	56	67.5	28	2	US-10-157-076-6	Sequence 6, Appl
45	56	67.5	28	2	US-10-157-076-12	Sequence 12, Appl
46	56	67.5	29	2	US-09-406-813-4	Sequence 4, Appl
47	56	67.5	29	2	US-09-843-221A-51	Sequence 51, Appl
48	56	67.5	29	2	US-09-843-221A-167	Sequence 167, App
49	56	67.5	30	1	US-08-262-495C-5	Sequence 5, Appl
50	56	67.5	30	1	US-08-262-495C-6	Sequence 6, Appl
51	56	67.5	30	2	US-08-904-760B-7	Sequence 7, Appl
52	56	67.5	30	2	US-08-904-760B-33	Sequence 33, Appl
53	56	67.5	30	2	US-08-904-760B-34	Sequence 34, Appl
54	56	67.5	30	2	US-08-904-760B-35	Sequence 35, Appl
55	56	67.5	30	2	US-09-536-785A-7	Sequence 7, Appl
56	56	67.5	30	2	US-09-536-785A-33	Sequence 33, Appl
57	56	67.5	30	2	US-09-536-785A-34	Sequence 34, Appl
58	56	67.5	30	2	US-09-536-785A-35	Sequence 35, Appl
59	56	67.5	30	2	US-09-843-221A-39	Sequence 39, Appl
60	56	67.5	30	2	US-09-843-221A-42	Sequence 42, Appl
61	56	67.5	30	2	US-09-843-221A-47	Sequence 47, Appl
62	56	67.5	30	2	US-09-843-221A-49	Sequence 49, Appl
63	56	67.5	30	2	US-09-843-221A-50	Sequence 50, Appl
64	56	67.5	30	2	US-09-843-221A-124	Sequence 124, App
65	56	67.5	30	2	US-09-843-221A-125	Sequence 125, App
66	56	67.5	30	2	US-09-843-221A-126	Sequence 126, App
67	56	67.5	30	2	US-09-843-221A-127	Sequence 127, App
68	56	67.5	30	2	US-09-843-221A-166	Sequence 166, App
69	56	67.5	31	1	US-08-262-495C-3	Sequence 3, Appl
70	56	67.5	31	1	US-08-262-495C-4	Sequence 4, Appl
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74	56	67.5	31	1	US-08-691-647C-4	Sequence 4, Appl
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76	56	67.5	31	2	US-08-904-760B-1	Sequence 1, Appl
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81	56	67.5	31	2	US-08-904-760B-6	Sequence 6, Appl
82	56	67.5	31	2	US-08-904-760B-8	Sequence 8, Appl
83	56	67.5	31	2	US-08-904-760B-11	Sequence 11, Appl
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85	56	67.5	31	2	US-08-904-760B-15	Sequence 15, Appl
86	56	67.5	31	2	US-08-904-760B-16	Sequence 16, Appl
87	56	67.5	31	2	US-08-904-760B-17	Sequence 17, Appl
88	56	67.5	31	2	US-08-904-760B-18	Sequence 18, Appl
89	56	67.5	31	2	US-08-904-760B-19	Sequence 19, Appl
90	56	67.5	31	2	US-08-904-760B-20	Sequence 20, Appl
91	56	67.5	31	2	US-08-904-760B-21	Sequence 21, Appl
92	56	67.5	31	2	US-08-904-760B-32	Sequence 32, Appl
93	56	67.5	31	2	US-09-406-813-2	Sequence 2, Appl
94	56	67.5	31	2	US-09-406-813-5	Sequence 5, Appl
95	56	67.5	31	2	US-09-536-785A-1	Sequence 1, Appl
96	56	67.5	31	2	US-09-536-785A-2	Sequence 2, Appl
97	56	67.5	31	2	US-09-536-785A-3	Sequence 3, Appl
98	56	67.5	31	2	US-09-536-785A-4	Sequence 4, Appl
99	56	67.5	31	2	US-09-536-785A-5	Sequence 5, Appl
100	56	67.5	31	2	US-09-536-785A-5	Sequence 5, Appl

## ALIGNMENTS

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RESULT 1
US-09-730-174A-5
; Sequence 5, Application US/09730174A
; Patent No. 6838264
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5
Query Match 71.1%; Score 59; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12

RESULT 2
US-09-421-379-5
; Sequence 5, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
; FILE REFERENCE: 0609.4570001
; CURRENT APPLICATION NUMBER: US/09/421,379
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: U.S. 60/105,530
; EARLIER FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-421-379-5
Query Match 71.1%; Score 59; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12

RESULT 3
US-09-730-174A-11

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; Sequence 11, Application US/09730174A
; Patent No. 6838264
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-11
Query Match 71.1%; Score 59; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12

RESULT 4
US-09-448-867-5
; Sequence 5, Application US/09448867
; Patent No. 6417333
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J
; APPLICANT: POTTS JR., JOHN T.
; TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION
; FILE REFERENCE: 0609.4640001
; CURRENT APPLICATION NUMBER: US/09/448,867
; CURRENT FILING DATE: 1999-11-24
; EARLIER APPLICATION NUMBER: 60/109,938
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-448-867-5
Query Match 71.1%; Score 59; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12

RESULT 5
US-09-448-867-9
; Sequence 9, Application US/09448867
; Patent No. 6417333
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J
; APPLICANT: POTTS JR., JOHN T.
; TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION
; FILE REFERENCE: 0609.4640001
; CURRENT APPLICATION NUMBER: US/09/448,867

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; CURRENT FILING DATE: 1999-11-24  
; EARLIER APPLICATION NUMBER: 60/109,938  
; EARLIER FILING DATE: 1998-11-25  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-448-867-9

Query Match 71.1%; Score 59; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 12  
Db 1 AVSEIQLMHNLG 12  
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RESULT 6  
US-09-447-800-7  
; Sequence 7, Application US/09447800  
; Patent No. 6537965  
; GENERAL INFORMATION:  
; APPLICANT: BRINGHURST, F. RICHARD  
; APPLICANT: TAKASU, HISASHI  
; APPLICANT: GARDELLA, THOMAS J.  
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)  
; FILE REFERENCE: 0609.4630001  
; CURRENT APPLICATION NUMBER: US/09/447,800  
; CURRENT FILING DATE: 1999-11-23  
; EARLIER APPLICATION NUMBER: 60/110,152  
; EARLIER FILING DATE: 1998-11-25  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Desamino Ala  
US-09-447-800-7

Query Match 71.1%; Score 59; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 12  
Db 1 AVSEIQLMHNLG 12  
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RESULT 7  
US-10-157-076-5  
; Sequence 5, Application US/10157076  
; Patent No. 6803213  
; GENERAL INFORMATION:  
; APPLICANT: BRINGHURST, F. RICHARD  
; APPLICANT: TAKASU, HISASHI  
; APPLICANT: GARDELLA, THOMAS J.  
; APPLICANT: POTTS, JOHN T. JR.  
; TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use  
; FILE REFERENCE: 0609.4640002  
; CURRENT APPLICATION NUMBER: US/10/157,076  
; CURRENT FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: US 09/448,867  
; PRIOR FILING DATE: 1999-11-24  
; PRIOR APPLICATION NUMBER: US 60/109,938  
; PRIOR FILING DATE: 1998-11-25

; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-157-076-5

Query Match 71.1%; Score 59; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 12  
Db 1 AVSEIQLMHNLG 12  
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RESULT 8  
US-10-157-076-9  
; Sequence 9, Application US/10157076  
; Patent No. 6803213  
; GENERAL INFORMATION:  
; APPLICANT: BRINGHURST, F. RICHARD  
; APPLICANT: TAKASU, HISASHI  
; APPLICANT: GARDELLA, THOMAS J.  
; APPLICANT: POTTS, JOHN T. JR.  
; TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use  
; FILE REFERENCE: 0609.4640002  
; CURRENT APPLICATION NUMBER: US/10/157,076  
; CURRENT FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: US 09/448,867  
; PRIOR FILING DATE: 1999-11-24  
; PRIOR APPLICATION NUMBER: US 60/109,938  
; PRIOR FILING DATE: 1998-11-25  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-157-076-9

Query Match 71.1%; Score 59; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 12  
Db 1 AVSEIQLMHNLG 12  
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RESULT 9  
US-09-448-867-4  
; Sequence 4, Application US/09448867  
; Patent No. 6417333  
; GENERAL INFORMATION:  
; APPLICANT: BRINGHURST, F. RICHARD  
; APPLICANT: TAKASU, HISASHI  
; APPLICANT: GARDELLA, THOMAS J.  
; APPLICANT: POTTS JR., JOHN T.  
; TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION  
; FILE REFERENCE: 0609.4640001  
; CURRENT APPLICATION NUMBER: US/09/448,867  
; CURRENT FILING DATE: 1999-11-24  
; EARLIER APPLICATION NUMBER: 60/109,938  
; EARLIER FILING DATE: 1998-11-25  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Homo sapiens

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US-09-448-867-4
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Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12
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RESULT 10
US-09-448-867-8
; Sequence 8, Application US/09448867
; Patent No. 6417333
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J
; APPLICANT: POTTS JR., JOHN T.
; TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION
; FILE REFERENCE: 0609.4640001
; CURRENT APPLICATION NUMBER: US/09/448,867
; CURRENT FILING DATE: 1999-11-24
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 28
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US-09-448-867-8

Query Match      71.1%; Score 59; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12
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RESULT 11
US-10-157-076-4
; Sequence 4, Application US/10157076
; Patent No. 6803213
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; APPLICANT: POTTS, JOHN T. JR.
; TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION AND USE
; FILE REFERENCE: 0609.4640002
; CURRENT APPLICATION NUMBER: US/10/157,076
; CURRENT FILING DATE: 2002-05-30
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: US 60/109,938
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-076-4

Query Match      71.1%; Score 59; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12
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RESULT 12
US-10-157-076-8
; Sequence 8, Application US/10157076
; Patent No. 6803213
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; APPLICANT: POTTS, JOHN T. JR.
; TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
; FILE REFERENCE: 0609.4640002
; CURRENT APPLICATION NUMBER: US/10/157,076
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 09/448,867
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: US 60/109,938
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-076-8

Query Match      71.1%; Score 59; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12
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RESULT 13
US-09-843-221A-48
; Sequence 48, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: KOSTENIUK, PAUL
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rat PTH
US-09-843-221A-48

Query Match      71.1%; Score 59; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
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Db 1 AVSEIQLMNLG 12

RESULT 14  
US-09-228-990-31  
Sequence 31, Application US/09228990  
Patent No. 6472505  
GENERAL INFORMATION:  
APPLICANT: Condon, Stephen M.  
APPLICANT: Morize, Isabelle  
TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, Mailstop 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/228,990  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/046,472  
FILING DATE: 14-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Martin Esq., Michael B.  
REGISTRATION NUMBER: 37,521  
REFERENCE/DOCKET NUMBER: A26788-WO  
TELEPHONE: (610) 454-2793  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 8  
OTHER INFORMATION: /product= "Nle"  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 18..22  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "The side chains of Lys at position 18 and Asp at position 22 are linked by an amide bond."  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 31  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "This C-terminal amino acid is an amide, i.e., CONH2."  
US-09-228-990-31

Query Match 71.1%; Score 59; DB 2; Length 31;  
Best Local Similarity 92.3%; Pred. No. 0.023;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQLMNLGG 13  
Db 1 AVSEIQLMNLGG 13

RESULT 15  
US-09-447-800-6  
Sequence 6, Application US/09447800  
Patent No. 6537965  
GENERAL INFORMATION:  
APPLICANT: BRINGHURST, F. RICHARD  
APPLICANT: TAKASU, HISASHI  
APPLICANT: GARDELLA, THOMAS J.  
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)  
TITLE OF INVENTION: ANALOGS  
FILE REFERENCE: 0609.4630001  
CURRENT APPLICATION NUMBER: US/09/447,800  
CURRENT FILING DATE: 1999-11-23  
EARLIER APPLICATION NUMBER: 60/110,152  
EARLIER FILING DATE: 1998-11-25  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
TYPE: PRT  
LENGTH: 33  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: Desamino Ala  
US-09-447-800-6

Query Match 71.1%; Score 59; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.025;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMNLG 12  
Db 1 AVSEIQLMNLG 12

RESULT 16  
US-08-488-105-3  
Sequence 3, Application US/08488105  
Patent No. 5717062  
GENERAL INFORMATION:  
APPLICANT: Chorev, Michael  
APPLICANT: Rosenblatt, Michael  
TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHrP  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,105  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Tsao, Y. Rocky  
REGISTRATION NUMBER: 34,053  
REFERENCE/DOCKET NUMBER: 00537/112001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid

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/ STRANDEDNESS: not relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ OTHER INFORMATION: The side chains of Lys at
/ position 13 and Asp at position 17 are linked by an amide bond
/ OTHER INFORMATION: and this sequence has an amide C-terminus (i.e., CONH2), rather
/ OTHER INFORMATION: than a carboxy C-terminus (i.e., COOH).
US-08-488-105-3
Query Match 71.1%; Score 59; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12
RESULT 17
US-08-488-105-9
; Sequence 9, Application US/08488105
; Patent No. 5717062
; GENERAL INFORMATION:
; APPLICANT: Chorev, Michael
; APPLICANT: Rosenblatt, Michael
; TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHrP
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,105
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Y. Rocky
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 00537/112001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: The side chains of Lys at
; position 26 and Asp at position 30 are linked by an amide bond
; OTHER INFORMATION: and this sequence has an amide C-terminus (i.e., CONH2), rather
; OTHER INFORMATION: than a carboxy C-terminus (i.e., COOH).
US-08-488-105-9
Query Match 71.1%; Score 59; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12
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RESULT 18
US-08-488-105-15
; Sequence 15, Application US/08488105
; Patent No. 5717062
; GENERAL INFORMATION:
; APPLICANT: Chorev, Michael
; APPLICANT: Rosenblatt, Michael
; TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHrP
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,105
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Y. Rocky
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 00537/112001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: The side chains of Lys at
; position 13 and Asp at position 17 and the side chains of Lys
; position 26 and Asp at position 30 are linked by an amide bond
; OTHER INFORMATION: and this sequence has an amide C-terminus (i.e., COOH).
US-08-488-105-15
Query Match 71.1%; Score 59; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12
RESULT 19
US-09-447-800-5
; Sequence 5, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; FILE REFERENCE: 0609,4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
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; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)_RES
; OTHER INFORMATION: Desamino Ala
US-09-447-800-5
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Query Match 71.1%; Score 59; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12
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# RESULT 20

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US-09-843-221A-25
; Sequence 25, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-843-221A-25
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Query Match 71.1%; Score 59; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12
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Search completed: November 21, 2005, 16:53:33
Job time : 47 secs
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OM protein - protein search, using sw model

Run on: November 21, 2005, 16:39:00 ; Search time 163 Seconds  
(without alignments)

41.014 Million cell updates/sec

Title: SEQ-NEW

Perfect score: 83

Sequence: 1 avseiqmhnlgggg 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	71.1	12	3	US-09-730-174A-5
2	59	71.1	12	5	US-10-998-927-5
3	59	71.1	13	3	US-09-898-398-3
4	59	71.1	13	5	US-10-921-368-3
5	59	71.1	14	4	US-10-192-673-5
6	59	71.1	15	3	US-09-730-174A-11
7	59	71.1	15	5	US-10-998-927-11
8	59	71.1	21	5	US-10-484-080-18
9	59	71.1	27	4	US-10-361-928-7
10	59	71.1	27	4	US-10-157-076-5
11	59	71.1	27	4	US-10-157-076-9
12	59	71.1	27	5	US-10-959-605-5
13	59	71.1	27	5	US-10-959-605-9
14	59	71.1	28	4	US-10-157-076-4
15	59	71.1	28	4	US-10-157-076-8
16	59	71.1	28	5	US-10-959-605-4
17	59	71.1	28	5	US-10-959-605-8
18	59	71.1	30	3	US-09-843-221A-48
19	59	71.1	30	3	US-09-999-608-48
20	59	71.1	30	4	US-10-839-037-48
21	59	71.1	31	4	US-10-097-079-31
22	59	71.1	33	4	US-10-361-928-6
23	59	71.1	34	3	US-09-843-221A-25
24	59	71.1	34	3	US-09-999-608-25
25	59	71.1	34	4	US-10-361-928-5
26	59	71.1	34	4	US-10-340-484-22
27	59	71.1	34	4	US-10-340-484-23

28	59	71.1	34	4	US-10-839-037-25	Sequence 25, Appl
29	59	71.1	34	5	US-10-428-377-46	Sequence 46, Appl
30	59	71.1	34	5	US-10-484-080-30	Sequence 30, Appl
31	59	71.1	34	5	US-10-638-265-87	Sequence 87, Appl
32	59	71.1	34	6	US-11-066-697-274	Sequence 274, App
33	59	71.1	34	6	US-09-843-221A-11	Sequence 11, Appl
34	59	71.1	84	3	US-09-999-608-11	Sequence 11, Appl
35	59	71.1	84	4	US-10-215-770-5	Sequence 5, Appl
36	59	71.1	84	4	US-10-398-449-16	Sequence 16, Appl
37	59	71.1	84	4	US-10-311-366-11	Sequence 11, Appl
38	59	71.1	84	4	US-10-839-037-11	Sequence 11, Appl
39	59	71.1	84	5	US-10-617-489-2	Sequence 2, Appl
40	59	71.1	84	5	US-10-617-489-3	Sequence 3, Appl
41	59	71.1	84	5	US-10-638-265-86	Sequence 86, Appl
42	57	68.7	31	4	US-10-097-079-32	Sequence 32, Appl
43	56	67.5	12	3	US-09-730-174A-3	Sequence 3, Appl
44	56	67.5	12	3	US-10-998-927-3	Sequence 3, Appl
45	56	67.5	13	3	US-09-898-398-4	Sequence 4, Appl
46	56	67.5	13	5	US-10-921-368-4	Sequence 4, Appl
47	56	67.5	14	4	US-10-192-673-3	Sequence 3, Appl
48	56	67.5	15	3	US-09-730-174A-9	Sequence 9, Appl
49	56	67.5	15	5	US-10-998-927-9	Sequence 9, Appl
50	56	67.5	21	5	US-10-484-080-17	Sequence 17, Appl
51	56	67.5	27	4	US-10-361-928-10	Sequence 10, Appl
52	56	67.5	27	4	US-10-157-076-7	Sequence 7, Appl
53	56	67.5	27	4	US-10-157-076-13	Sequence 13, Appl
54	56	67.5	27	5	US-10-959-605-7	Sequence 7, Appl
55	56	67.5	27	5	US-10-959-605-13	Sequence 13, Appl
56	56	67.5	28	3	US-09-843-221A-52	Sequence 52, Appl
57	56	67.5	28	3	US-09-843-221A-168	Sequence 168, App
58	56	67.5	28	3	US-09-999-608-52	Sequence 52, Appl
59	56	67.5	28	4	US-10-157-076-6	Sequence 6, Appl
60	56	67.5	28	4	US-10-157-076-12	Sequence 12, Appl
61	56	67.5	28	4	US-10-839-037-52	Sequence 52, Appl
62	56	67.5	28	4	US-10-839-037-168	Sequence 168, App
63	56	67.5	28	5	US-10-959-605-6	Sequence 6, Appl
64	56	67.5	28	5	US-10-959-605-12	Sequence 12, Appl
65	56	67.5	29	3	US-09-843-221A-51	Sequence 51, Appl
66	56	67.5	29	3	US-09-843-221A-167	Sequence 167, App
67	56	67.5	29	3	US-09-999-608-51	Sequence 51, Appl
68	56	67.5	29	4	US-10-839-037-51	Sequence 51, Appl
69	56	67.5	29	4	US-10-839-037-167	Sequence 167, App
70	56	67.5	30	3	US-09-843-221A-39	Sequence 39, Appl
71	56	67.5	30	3	US-09-843-221A-42	Sequence 42, Appl
72	56	67.5	30	3	US-09-843-221A-47	Sequence 47, Appl
73	56	67.5	30	3	US-09-843-221A-49	Sequence 49, Appl
74	56	67.5	30	3	US-09-843-221A-50	Sequence 50, Appl
75	56	67.5	30	3	US-09-843-221A-124	Sequence 124, App
76	56	67.5	30	3	US-09-843-221A-125	Sequence 125, App
77	56	67.5	30	3	US-09-843-221A-126	Sequence 126, App
78	56	67.5	30	3	US-09-843-221A-127	Sequence 127, App
79	56	67.5	30	3	US-09-843-221A-166	Sequence 166, App
80	56	67.5	30	3	US-09-999-608-39	Sequence 39, Appl
81	56	67.5	30	3	US-09-999-608-42	Sequence 42, Appl
82	56	67.5	30	3	US-09-999-608-47	Sequence 47, Appl
83	56	67.5	30	3	US-09-999-608-49	Sequence 49, Appl
84	56	67.5	30	3	US-09-999-608-50	Sequence 50, Appl
85	56	67.5	30	3	US-09-999-608-124	Sequence 124, App
86	56	67.5	30	3	US-09-999-608-125	Sequence 125, App
87	56	67.5	30	3	US-09-999-608-126	Sequence 126, App
88	56	67.5	30	3	US-09-999-608-127	Sequence 127, App
89	56	67.5	30	3	US-09-999-608-166	Sequence 166, App
90	56	67.5	30	4	US-10-398-449-5	Sequence 5, Appl
91	56	67.5	30	4	US-10-839-037-39	Sequence 39, Appl
92	56	67.5	30	4	US-10-839-037-42	Sequence 42, Appl
93	56	67.5	30	4	US-10-839-037-47	Sequence 47, Appl
94	56	67.5	30	4	US-10-839-037-49	Sequence 49, Appl
95	56	67.5	30	4	US-10-839-037-50	Sequence 50, Appl
96	56	67.5	30	4	US-10-839-037-124	Sequence 124, App
97	56	67.5	30	4	US-10-839-037-125	Sequence 125, App
98	56	67.5	30	4	US-10-839-037-126	Sequence 126, App
99	56	67.5	30	4	US-10-839-037-127	Sequence 127, App
100	56	67.5	30	4	US-10-839-037-166	Sequence 166, App

## ALIGNMENTS

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RESULT 1
US-09-730-174A-5
; Sequence 5, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5

Query Match          71.1%; Score 59; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
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Db 1 AVSEIQLMHNLG 12

RESULT 2
US-10-998-927-5
; Sequence 5, Application US/10998927
; Publication No. US20050095236A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, Richard J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMMUNE-001B
; CURRENT APPLICATION NUMBER: US/10/998,927
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: US 09/730,174
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates Said Antibodies
US-10-998-927-5

Query Match          71.1%; Score 59; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
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Db 1 AVSEIQLMHNLG 12

RESULT 3
US-09-898-398-3
; Sequence 3, Application US/09898398
; Publication No. US20030082179A1
; GENERAL INFORMATION:
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; APPLICANT: Hutchison, James Scott
; TITLE OF INVENTION: PARATHYROID HORMONE ANTIBODIES AND RELATED METHODS
; FILE REFERENCE: A1713
; CURRENT APPLICATION NUMBER: US/09/898,398
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-398-3

Query Match          71.1%; Score 59; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
   |||||
Db 1 AVSEIQLMHNLG 12

RESULT 4
US-10-921-368-3
; Sequence 3, Application US/10921368
; Publication No. US20050003493A1
; GENERAL INFORMATION:
; APPLICANT: Hutchison, James Scott
; TITLE OF INVENTION: PARATHYROID HORMONE ANTIBODIES AND RELATED METHODS
; FILE REFERENCE: A1713
; CURRENT APPLICATION NUMBER: US/10/921,368
; CURRENT FILING DATE: 2004-08-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-921-368-3

Query Match          71.1%; Score 59; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
   |||||
Db 1 AVSEIQLMHNLG 12

RESULT 5
US-10-192-673-5
; Sequence 5, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John I.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; FILE REFERENCE: 0609.4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: U.S. 60/105,530
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-192-673-5

Query Match          71.1%; Score 59; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AVSEIQLMHNLG 12
Db      1 AVSEIQLMHNLG 12
        |||||
RESULT 6
US-09-730-174A-11
; Sequence 11, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-11

Query Match          71.1%; Score 59; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AVSEIQLMHNLG 12
Db      1 AVSEIQLMHNLG 12
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RESULT 7
US-10-998-927-11
; Sequence 11, Application US/10998927
; Publication No. US20050095236A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, Richard J.
; APPLICANT: Lavigne, Jeffrey R.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid
; TITLE OF INVENTION: Hormone (PTH) 1-84
; FILE REFERENCE: IMUNE-001B
; CURRENT APPLICATION NUMBER: US/10/998,927
; CURRENT FILING DATE: 2004-11-29
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 09/730,174
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates Said Antibodies
US-10-998-927-11

Query Match          71.1%; Score 59; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 AVSEIQLMHNLG 12
Db      1 AVSEIQLMHNLG 12
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RESULT 8
US-10-484-080-18
; Sequence 18, Application US/10484080
; Publication No. US20050026839A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; TITLE OF INVENTION: Conformationally Constrained Parathyroid
; TITLE OF INVENTION: Hormone (PTH) Analogs
; FILE REFERENCE: 0609.5110002
; CURRENT APPLICATION NUMBER: US/10/484,080
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/22922
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/326,212
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/306,866
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Rattus sp.
; OTHER INFORMATION:
US-10-484-080-18

Query Match          71.1%; Score 59; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AVSEIQLMHNLG 12
Db      1 AVSEIQLMHNLG 12
        |||||
RESULT 9
US-10-361-928-7
; Sequence 7, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-10-361-928-7

Query Match          71.1%; Score 59; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AVSEIQLMHNLG 12
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Db      1 AVSEIQLMHNLG 12
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RESULT 10
US-10-157-076-5
; Sequence 5, Application US/10157076
; Publication No. US20040176568A1
; GENERAL INFORMATION:
; APPLICANT: Bringham, F. Richard
; APPLICANT: Takasu, Hisashi
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Potts, John T. Jr.
; TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation
; FILE REFERENCE: 0609.4640002
; CURRENT APPLICATION NUMBER: US/10/959.605
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: US/10/157.076
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 09/448,867
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: US 60/109,938
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-076-5
Query Match      71.1%; Score 59; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AVSEIQLMHNLG 12
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Db      1 AVSEIQLMHNLG 12
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RESULT 11
US-10-157-076-9
; Sequence 9, Application US/10157076
; Publication No. US20040176568A1
; GENERAL INFORMATION:
; APPLICANT: Bringham, F. Richard
; APPLICANT: Takasu, Hisashi
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Potts, John T. Jr.
; TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
; FILE REFERENCE: 0609.4640002
; CURRENT APPLICATION NUMBER: US/10/157.076
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 09/448,867
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: US 60/109,938
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-076-9
Query Match      71.1%; Score 59; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AVSEIQLMHNLG 12
|||||
Db      1 AVSEIQLMHNLG 12
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RESULT 12
US-10-959-605-5
; Sequence 5, Application US/10959605
; Publication No. US20050203012A1
; GENERAL INFORMATION:
; APPLICANT: Bringham, F. Richard
; APPLICANT: Takasu, Hisashi
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Potts, John T. Jr.
; TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation
; FILE REFERENCE: 0609.4640002
; CURRENT APPLICATION NUMBER: US/10/959.605
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: US/10/157.076
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 09/448,867
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: US 60/109,938
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-605-5
Query Match      71.1%; Score 59; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AVSEIQLMHNLG 12
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Db      1 AVSEIQLMHNLG 12
|||||

RESULT 13
US-10-959-605-9
; Sequence 9, Application US/10959605
; Publication No. US20050203012A1
; GENERAL INFORMATION:
; APPLICANT: Bringham, F. Richard
; APPLICANT: Takasu, Hisashi
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Potts, John T. Jr.
; TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation
; FILE REFERENCE: 0609.4640002
; CURRENT APPLICATION NUMBER: US/10/959.605
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: US/10/157.076
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 09/448,867
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: US 60/109,938
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-605-9
Query Match      71.1%; Score 59; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AVSEIQLMHNLG 12
|||||
Db      1 AVSEIQLMHNLG 12
|||||

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RESULT 14  
 US-10-157-076-4  
 ; Sequence 4, Application US/10157076  
 ; Publication No. US20040176568A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bringhurst, F. Richard  
 ; APPLICANT: Takasu, Hisashi  
 ; APPLICANT: Gardella, Thomas J.  
 ; APPLICANT: Potts, John T. Jr.  
 ; TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use  
 ; FILE REFERENCE: 0609.4640002  
 ; CURRENT APPLICATION NUMBER: US/10/157,076  
 ; CURRENT FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: US 09/448,867  
 ; PRIOR FILING DATE: 1999-11-24  
 ; PRIOR APPLICATION NUMBER: US 60/109,938  
 ; PRIOR FILING DATE: 1998-11-25  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 28  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-157-076-4

Query Match 71.1%; Score 59; DB 4; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AVSEIQLMHNLG 12  
 |||||  
 Db 1 AVSEIQLMHNLG 12

RESULT 15  
 US-10-157-076-8  
 ; Sequence 8, Application US/10157076  
 ; Publication No. US20040176568A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bringhurst, F. Richard  
 ; APPLICANT: Takasu, Hisashi  
 ; APPLICANT: Gardella, Thomas J.  
 ; APPLICANT: Potts, John T. Jr.  
 ; TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use  
 ; FILE REFERENCE: 0609.4640002  
 ; CURRENT APPLICATION NUMBER: US/10/157,076  
 ; CURRENT FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: US 09/448,867  
 ; PRIOR FILING DATE: 1999-11-24  
 ; PRIOR APPLICATION NUMBER: US 60/109,938  
 ; PRIOR FILING DATE: 1998-11-25  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 8  
 ; LENGTH: 28  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-157-076-8

Query Match 71.1%; Score 59; DB 4; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AVSEIQLMHNLG 12  
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 Db 1 AVSEIQLMHNLG 12

RESULT 16  
 US-10-959-605-4  
 ; Sequence 4, Application US/10959605  
 ; Publication No. US20050203012A1  
 ; GENERAL INFORMATION:

; APPLICANT: Bringhurst, F. Richard  
 ; APPLICANT: Takasu, Hisashi  
 ; APPLICANT: Gardella, Thomas J.  
 ; APPLICANT: Potts, John T. Jr.  
 ; TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation  
 ; FILE REFERENCE: 0609.4640002  
 ; CURRENT APPLICATION NUMBER: US/10/959,605  
 ; CURRENT FILING DATE: 2004-10-07  
 ; PRIOR APPLICATION NUMBER: US/10/157,076  
 ; PRIOR FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: US 09/448,867  
 ; PRIOR FILING DATE: 1999-11-24  
 ; PRIOR APPLICATION NUMBER: US 60/109,938  
 ; PRIOR FILING DATE: 1998-11-25  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 28  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-959-605-4

Query Match 71.1%; Score 59; DB 5; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AVSEIQLMHNLG 12  
 |||||  
 Db 1 AVSEIQLMHNLG 12

RESULT 17  
 US-10-959-605-8  
 ; Sequence 8, Application US/10959605  
 ; Publication No. US20050203012A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bringhurst, F. Richard  
 ; APPLICANT: Takasu, Hisashi  
 ; APPLICANT: Gardella, Thomas J.  
 ; APPLICANT: Potts, John T. Jr.  
 ; TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation  
 ; FILE REFERENCE: 0609.4640002  
 ; CURRENT APPLICATION NUMBER: US/10/959,605  
 ; CURRENT FILING DATE: 2004-10-07  
 ; PRIOR APPLICATION NUMBER: US/10/157,076  
 ; PRIOR FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: US 09/448,867  
 ; PRIOR FILING DATE: 1999-11-24  
 ; PRIOR APPLICATION NUMBER: US 60/109,938  
 ; PRIOR FILING DATE: 1998-11-25  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 8  
 ; LENGTH: 28  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-959-605-8

Query Match 71.1%; Score 59; DB 5; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AVSEIQLMHNLG 12  
 |||||  
 Db 1 AVSEIQLMHNLG 12

RESULT 18  
 US-09-843-221A-48  
 ; Sequence 48, Application US/09843221A  
 ; Publication No. US20030039654A1

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; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; PRIOR FILING DATE: 2001-04-26
; PRIOR FILING DATE: 2001-02-06
; PRIOR FILING DATE: 2001-02-06
; PRIOR FILING DATE: 2000-06-28
; PRIOR FILING DATE: 2000-06-28
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rat PTH
US-09-843-221A-48

Query Match          71.1%; Score 59; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12

RESULT 19
US-09-999-608-48
; Sequence 48, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: GEGG, COLIN V.
; APPLICANT: JAROSINSKI, MARK ANTHONY
; APPLICANT: KINSTLER, OLAF BORIS
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
; TITLE OF INVENTION: HORMONE-RELATED PROTEIN
; FILE REFERENCE: A-665C
; CURRENT APPLICATION NUMBER: US/09/999,608
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/843,221
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rat PTH
US-09-999-608-48

Query Match          71.1%; Score 59; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12

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RESULT 20
US-10-839-037-48
; Sequence 48, Application US/10839037
; Publication No. US20040214996A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/10/839,037
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: US/09/843,221A
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rat PTH
US-10-839-037-48

Query Match          71.1%; Score 59; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12

Search completed: November 21, 2005, 16:56:22
Job time : 164 secs

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QM protein - protein search, using sw model

Run on: November 21, 2005, 16:43:05 ; Search time 6 Seconds  
(without alignments)  
3.013 Million cell updates/sec

Title: SEQ-NEW

Perfect score: 83

Sequence: 1 aveeiqlmhnlgggg 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %		Length	DB ID	Description
		Match				
1	47	56.6	28	1	US-10-939-890-464	Sequence 464, App
2	47	56.6	28	1	US-10-939-890-720	Sequence 720, App
3	47	56.6	28	1	US-10-939-890-723	Sequence 723, App
4	44	53.0	28	1	US-10-939-890-353	Sequence 353, App
5	44	53.0	28	1	US-10-939-890-829	Sequence 829, App
6	42	50.6	27	1	US-10-939-890-354	Sequence 354, App
7	42	50.6	27	1	US-10-939-890-830	Sequence 830, App
8	38	45.8	28	1	US-10-939-890-346	Sequence 346, App
9	38	45.8	28	1	US-10-939-890-383	Sequence 383, App
10	38	45.8	28	1	US-10-939-890-699	Sequence 699, App
11	38	45.8	28	1	US-10-939-890-822	Sequence 822, App
12	37.5	45.2	114	1	US-10-972-587-37	Sequence 37, Appli
13	37	44.6	27	1	US-10-939-890-700	Sequence 700, App
14	37	44.6	28	1	US-10-939-890-384	Sequence 384, App
15	37	44.6	368	1	US-10-689-742-100	Sequence 100, App
16	35	42.2	431	7	US-11-169-013-2	Sequence 2, Appli
17	35	42.2	2047	7	US-11-013-759-4	Sequence 4, Appli
18	35	42.2	2047	7	US-11-013-759-9	Sequence 7, Appli
19	35	42.2	2053	7	US-11-013-759-9	Sequence 9, Appli
20	34	41.0	28	1	US-10-939-890-325	Sequence 325, App
21	34	41.0	28	1	US-10-939-890-351	Sequence 351, App
22	34	41.0	28	1	US-10-939-890-827	Sequence 827, App
23	34	41.0	29	1	US-10-939-890-350	Sequence 350, App
24	34	41.0	29	1	US-10-939-890-381	Sequence 381, App
25	34	41.0	29	1	US-10-939-890-697	Sequence 697, App

Sequence 826, App  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 751, App  
Sequence 752, App  
Sequence 762, App  
Sequence 356, App  
Sequence 630, App  
Sequence 719, App  
Sequence 721, App  
Sequence 722, App  
Sequence 794, App  
Sequence 795, App  
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Sequence 847, App  
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Sequence 340, App  
Sequence 2, Appli

Sequence 6, Appl1  
Sequence 334, App

## ALIGNMENTS

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RESULT 1
US-10-939-890-464
; Sequence 464, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US 10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 464
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Library Isolate
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
; US-10-939-890-464
;
Query Match          56.6%; Score 47; DB 1; Length 28;
Best Local Similarity 57.1%; Pred. No. 0.02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

```

OY 3 SEIQLMHNLGGGG 16
Db 14 ADLQLSHFAGGGGG 27

```

```

RESULT 2
US-10-939-890-720
; Sequence 720, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.

```

```

; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US 10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 720
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
; US-10-939-890-720
;
Query Match          56.6%; Score 47; DB 1; Length 28;
Best Local Similarity 57.1%; Pred. No. 0.02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

```

OY 3 SEIQLMHNLGGGG 16
Db 14 ADLQLSHFAGGGGG 27

```

```

RESULT 3
US-10-939-890-723
; Sequence 723, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.

```

```

; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 723
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; FEATURE:
; OTHER INFORMATION: ACETYLATION
; NAME/KEY: MOD RES
; LOCATION: (28)-(28)
; OTHER INFORMATION: Lys residue modified with a SATA linker
US-10-939-890-723

Query Match 56.6%; Score 47; DB 1; Length 28;
Best Local Similarity 57.1%; Pred. No. 0.02;
Matches 8; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

```

```

Qy 3 SEIQLMHNLGGGG 16
Db 14 ADQLSHFAGGGG 27

RESULT 4
US-10-939-890-353
; Sequence 353, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

```

```

; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 353
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-353

Query Match 53.0%; Score 44; DB 1; Length 28;
Best Local Similarity 70.0%; Pred. No. 0.057;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 7 LMENLGGGG 16
Db 18 MFHQLGGGG 27

RESULT 5
US-10-939-890-829
; Sequence 829, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 829

```

```
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-829
```

```
Query Match 53.0%; Score 44; DB 1; Length 28;
Best Local Similarity 70.0%; Pred. No. 0.057;
Matches 7; Conservative 1; Mismatches 0; Indels 2; Gaps 0;
```

```
Oy 7 LMHNLGGGGG 16
    :|||
Db 18 MFHOLGGGGG 27
```

```
RESULT 6
US-10-939-890-354
; Sequence 354, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/939,890
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 354
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (27)..(27)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-830
```

```
Query Match 50.6%; Score 42; DB 1; Length 27;
Best Local Similarity 53.8%; Pred. No. 0.11;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy 4 EIOLMNLGGGG 16
    :|||
Db 14 EVELVDHPGGGG 26
```

```
Best Local Similarity 53.8%; Pred. No. 0.11;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 4 EIOLMNLGGGG 16
    :|||
Db 14 EVELVDHPGGGG 26
```

```
RESULT 7
US-10-939-890-830
; Sequence 830, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/939,890
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 830
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (27)..(27)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-830
```

```
Query Match 50.6%; Score 42; DB 1; Length 27;
Best Local Similarity 53.8%; Pred. No. 0.11;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy 4 EIOLMNLGGGG 16
    :|||
Db 14 EVELVDHPGGGG 26
```



## RESULT 8

US-10-939-890-346

; Sequence 346, Application US/10939890

; Publication No. US20050250700A1

; GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.

; APPLICANT: Sexton, Daniel J.

; APPLICANT: Dransfield, Daniel T.

; APPLICANT: Ladner, Robert C.

; APPLICANT: Arbogast, Christophe

; APPLICANT: Bussat, Philippe

; APPLICANT: Fan, Hong

; APPLICANT: Khurana, Sudha

; APPLICANT: Linder, Karen E.

; APPLICANT: Marinelli, Edmund R.

; APPLICANT: Nanjappan, Palaniappa

; APPLICANT: Nunn, Adrian D.

; APPLICANT: Pillai, Radhakrishna

; APPLICANT: Pochon, Sibylle

; APPLICANT: Ramalingam, Kondareddiar

; APPLICANT: Shrivastava, Ajay

; APPLICANT: Song, Bo

; APPLICANT: Swenson, Rolf E.

; APPLICANT: Von Wronski, Mathew A.

; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

; FILE REFERENCE: D0617.70014US00

; CURRENT APPLICATION NUMBER: US/10/939,890

; CURRENT FILING DATE: 2004-09-13

; PRIOR APPLICATION NUMBER: US 10/661,156

; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: PCT/US03/06731

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/440,411

; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/360,851

; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 883

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 346

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide

US-10-939-890-346

Query Match 45.8%; Score 38; DB 1; Length 28;

Best Local Similarity 70.0%; Pred. No. 0.48;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY

7 LMHNLGSGGG 16

| | | | |

18 LNHSFGGGG 27

| | | | |

Db

RESULT 9

US-10-939-890-383

; Sequence 383, Application US/10939890

; Publication No. US20050250700A1

; GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.

; APPLICANT: Sexton, Daniel J.

; APPLICANT: Dransfield, Daniel T.

; APPLICANT: Ladner, Robert C.

; APPLICANT: Arbogast, Christophe

; APPLICANT: Bussat, Philippe

; APPLICANT: Fan, Hong

; APPLICANT: Khurana, Sudha

; APPLICANT: Linder, Karen E.

; APPLICANT: Marinelli, Edmund R.

; APPLICANT: Nanjappan, Palaniappa

; APPLICANT: Nunn, Adrian D.  
; APPLICANT: Pillai, Radhakrishna  
; APPLICANT: Pochon, Sibylle  
; APPLICANT: Ramalingam, Kondareddiar  
; APPLICANT: Shrivastava, Ajay  
; APPLICANT: Song, Bo  
; APPLICANT: Swenson, Rolf E.  
; APPLICANT: Von Wronski, Mathew A.

; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

; FILE REFERENCE: D0617.70014US00

; CURRENT APPLICATION NUMBER: US/10/939,890

; CURRENT FILING DATE: 2004-09-13

; PRIOR APPLICATION NUMBER: US 10/661,156

; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: PCT/US03/06731

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/440,411

; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/360,851

; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 883

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 383

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Library Isolate

US-10-939-890-383

Query Match 45.8%; Score 38; DB 1; Length 28;

Best Local Similarity 70.0%; Pred. No. 0.48;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY

7 LMHNLGSGGG 16

| | | | |

18 LNHSFGGGG 27

| | | | |

Db

RESULT 10

US-10-939-890-699

; Sequence 699, Application US/10939890

; Publication No. US20050250700A1

; GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.

; APPLICANT: Sexton, Daniel J.

; APPLICANT: Dransfield, Daniel T.

; APPLICANT: Ladner, Robert C.

; APPLICANT: Arbogast, Christophe

; APPLICANT: Bussat, Philippe

; APPLICANT: Fan, Hong

; APPLICANT: Khurana, Sudha

; APPLICANT: Linder, Karen E.

; APPLICANT: Marinelli, Edmund R.

; APPLICANT: Nanjappan, Palaniappa

; APPLICANT: Nunn, Adrian D.

; APPLICANT: Pillai, Radhakrishna

; APPLICANT: Pochon, Sibylle

; APPLICANT: Ramalingam, Kondareddiar

; APPLICANT: Shrivastava, Ajay

; APPLICANT: Song, Bo

; APPLICANT: Swenson, Rolf E.

; APPLICANT: Von Wronski, Mathew A.

; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

; FILE REFERENCE: D0617.70014US00

; CURRENT APPLICATION NUMBER: US/10/939,890

; CURRENT FILING DATE: 2004-09-13

; PRIOR APPLICATION NUMBER: US 10/661,156

; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082

; PRIOR FILING DATE: 2003-03-03

```

; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 699
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-699

Query Match 45.8%; Score 38; DB 1; Length 28;
Best Local Similarity 70.0%; Pred. No. 0.48;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 LMHNLGCGG 16
Db 18 LNHSPGGGG 27

RESULT 11
US-10-939-890-822
; Sequence 822, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Buesat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617, 70014US09
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 822
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; NAME/KEY: MOD_RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-822

Query Match 45.8%; Score 38; DB 1; Length 28;
Best Local Similarity 70.0%; Pred. No. 0.48;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 LMHNLGCGG 16
Db 18 LNHSPGGGG 27

RESULT 12
US-10-972-587-37
; Sequence 37, Application US/10972587
; Publication No. US20050246799A1
; GENERAL INFORMATION:
; APPLICANT: Song, Xiaoling
; APPLICANT: Bariola, Pauline Anne
; APPLICANT: Linderoth, Nora Abiella
; APPLICANT: Fan, Hao
; APPLICANT: Wei, Zhong-Min
; TITLE OF INVENTION: RECEPTORS FOR HYPERSENSITIVE RESPONSE ELICITORS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 21829/213
; CURRENT APPLICATION NUMBER: US/10/972,587
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: 60/335,776
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 09/810,997
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 10/174,209
; PRIOR FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Xanthomonas campestris pv. pelargonii
US-10-972-587-37

Query Match 45.2%; Score 37.5; DB 1; Length 114;
Best Local Similarity 60.0%; Pred. No. 2.4;
Matches 9; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 5 IOLMHNLGCGG 16
Db 89 MQLMQGGGAGMG 103

RESULT 13
US-10-939-890-700
; Sequence 700, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.

```

APPLICANT: Sexton, Daniel J.  
 APPLICANT: Dransfield, Daniel T.  
 APPLICANT: Ladner, Robert C.  
 APPLICANT: Arbogast, Christophe  
 APPLICANT: Bussat, Philippe  
 APPLICANT: Fan, Hong  
 APPLICANT: Khurana, Sudha  
 APPLICANT: Linder, Karen E.  
 APPLICANT: Marinelli, Edmund R.  
 APPLICANT: Nanjappan, Palaniappa  
 APPLICANT: Nunn, Adrian D.  
 APPLICANT: Pillai, Radhakrishna  
 APPLICANT: Pochon, Sibylle  
 APPLICANT: Ramalingam, Kondareddiar  
 APPLICANT: Shrivastava, Ajay  
 APPLICANT: Song, Bo  
 APPLICANT: Swenson, Rolf E.  
 APPLICANT: Von Wronski, Mathew A.  
 TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES  
 FILE REFERENCE: D0617.70014US00  
 CURRENT APPLICATION NUMBER: US/10/939,890  
 CURRENT FILING DATE: 2004-09-13  
 PRIOR APPLICATION NUMBER: US 10/661,156  
 PRIOR FILING DATE: 2003-09-11  
 PRIOR APPLICATION NUMBER: US 10/382,082  
 PRIOR FILING DATE: 2003-03-03  
 PRIOR APPLICATION NUMBER: PCT/US03/06731  
 PRIOR FILING DATE: 2003-03-03  
 PRIOR APPLICATION NUMBER: US 60/440,411  
 PRIOR FILING DATE: 2003-01-15  
 PRIOR APPLICATION NUMBER: US 60/360,851  
 PRIOR FILING DATE: 2002-03-01  
 NUMBER OF SEQ ID NOS: 883  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 700  
 LENGTH: 27  
 TYPE: PRT  
 ORGANISM: Artificial sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic peptide  
 NAME/KEY: MOD RES  
 LOCATION: (1)..(1)  
 OTHER INFORMATION: ACETYLATION  
 NAME/KEY: MOD RES  
 LOCATION: (27)..(27)  
 OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker  
 US-10-939-890-700

Query Match 44.6%; Score 37; DB 1; Length 27;  
 Best Local Similarity 85.7%; Pred. No. 0.65;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGGGGG 16  
 Db 20 NVGGGGG 26

RESULT 14  
 US-10-939-890-384  
 Sequence 384, Application US/10939890  
 Publication No. US20050250700A1  
 GENERAL INFORMATION:  
 APPLICANT: Sato, Aaron K.  
 APPLICANT: Sexton, Daniel J.  
 APPLICANT: Dransfield, Daniel T.  
 APPLICANT: Ladner, Robert C.  
 APPLICANT: Arbogast, Christophe  
 APPLICANT: Bussat, Philippe  
 APPLICANT: Fan, Hong  
 APPLICANT: Khurana, Sudha  
 APPLICANT: Linder, Karen E.

APPLICANT: Marinelli, Edmund R.  
 APPLICANT: Nanjappan, Palaniappa  
 APPLICANT: Nunn, Adrian D.  
 APPLICANT: Pillai, Radhakrishna  
 APPLICANT: Pochon, Sibylle  
 APPLICANT: Ramalingam, Kondareddiar  
 APPLICANT: Shrivastava, Ajay  
 APPLICANT: Song, Bo  
 APPLICANT: Swenson, Rolf E.  
 APPLICANT: Von Wronski, Mathew A.  
 TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES  
 FILE REFERENCE: D0617.70014US00  
 CURRENT APPLICATION NUMBER: US/10/939,890  
 CURRENT FILING DATE: 2004-09-13  
 PRIOR APPLICATION NUMBER: US 10/661,156  
 PRIOR FILING DATE: 2003-09-11  
 PRIOR APPLICATION NUMBER: US 10/382,082  
 PRIOR FILING DATE: 2003-03-03  
 PRIOR APPLICATION NUMBER: PCT/US03/06731  
 PRIOR FILING DATE: 2003-03-03  
 PRIOR APPLICATION NUMBER: US 60/440,411  
 PRIOR FILING DATE: 2003-01-15  
 PRIOR APPLICATION NUMBER: US 60/360,851  
 PRIOR FILING DATE: 2002-03-01  
 NUMBER OF SEQ ID NOS: 883  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 384  
 LENGTH: 28  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Library Isolate  
 US-10-939-890-384

Query Match 44.6%; Score 37; DB 1; Length 28;  
 Best Local Similarity 85.7%; Pred. No. 0.68;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGGGGG 16  
 Db 21 NVGGGGG 27

RESULT 15  
 US-10-689-742-100  
 Sequence 100, Application US/10689742  
 Publication No. US20050250180A1  
 GENERAL INFORMATION:  
 APPLICANT: Jacobs, Kenneth  
 APPLICANT: McCoy, John M  
 APPLICANT: Lavallie, Edward R  
 APPLICANT: Racie, Lisa A  
 APPLICANT: Evans, Cheryl  
 APPLICANT: Merberg, David  
 APPLICANT: Treacy, Maurice  
 APPLICANT: Spaulding, Vikki  
 TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
 FILE REFERENCE: 00766.000091.10  
 CURRENT APPLICATION NUMBER: US/10/689,742  
 CURRENT FILING DATE: 2003-10-22  
 PRIOR APPLICATION NUMBER: 09/746,783  
 PRIOR FILING DATE: 2000-12-21  
 NUMBER OF SEQ ID NOS: 231  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 100  
 LENGTH: 368  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-689-742-100

Query Match 44.6%; Score 37; DB 1; Length 368;  
 Best Local Similarity 53.8%; Pred. No. 9.7;  
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLCGG 14  
Db 59 VNSLQKQKNGGG 71

RESULT 16  
US-11-169-013-2  
; Sequence 2, Application US/11169013  
; Publication No. US20050244971A1  
; GENERAL INFORMATION:  
; APPLICANT: Korea Kumho Petrochemical Co., Ltd.  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH ENHANCED STRESS TOLERANCE  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/11/169,013  
; CURRENT FILING DATE: 2005-06-29  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 2  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-11-169-013-2

Query Match 42.2%; Score 35; DB 7; Length 431;  
Best Local Similarity 85.7%; Pred. No. 23;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 HNLGGGG 15  
Db 8 NNLGGGG 14

RESULT 17  
US-11-013-759-4  
; Sequence 4, Application US/11013759  
; Publication No. US20050249747A1  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M.  
; APPLICANT: Sasaki, Ken  
; APPLICANT: Yang, Yan Ping  
; APPLICANT: Klein, Michel H.  
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE  
; FILE REFERENCE: 1038-921MIS:jb  
; CURRENT APPLICATION NUMBER: US/11/013,759  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 2047  
; TYPE: PRT  
; ORGANISM: Moraxella catarrhalis  
US-11-013-759-4

Query Match 42.2%; Score 35; DB 7; Length 2047;  
Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLCGG 14  
Db 18 AVAEYAKSHSTGGG 31

RESULT 18  
US-11-013-759-7  
; Sequence 7, Application US/11013759  
; Publication No. US20050249747A1  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M.  
; APPLICANT: Sasaki, Ken

; APPLICANT: Yang, Yan Ping  
; APPLICANT: Klein, Michel H.  
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE  
; FILE REFERENCE: 1038-921MIS:jb  
; CURRENT APPLICATION NUMBER: US/11/013,759  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 2047  
; TYPE: PRT  
; ORGANISM: Moraxella catarrhalis  
US-11-013-759-7

Query Match 42.2%; Score 35; DB 7; Length 2047;  
Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLCGG 14  
Db 18 AVAEYAKSHSTGGG 31

RESULT 19  
US-11-013-759-9  
; Sequence 9, Application US/11013759  
; Publication No. US20050249747A1  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M.  
; APPLICANT: Sasaki, Ken  
; APPLICANT: Yang, Yan Ping  
; APPLICANT: Klein, Michel H.  
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE  
; FILE REFERENCE: 1038-921MIS:jb  
; CURRENT APPLICATION NUMBER: US/11/013,759  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 2053  
; TYPE: PRT  
; ORGANISM: Moraxella catarrhalis  
US-11-013-759-9

Query Match 42.2%; Score 35; DB 7; Length 2053;  
Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLCGG 14  
Db 18 AVAEYAKSHSTGGG 31

RESULT 20  
US-10-939-890-325  
; Sequence 325, Application US/10939890  
; Publication No. US20050250700A1  
; GENERAL INFORMATION:  
; APPLICANT: Sato, Aaron K.  
; APPLICANT: Sexton, Daniel J.  
; APPLICANT: Dransfield, Daniel T.  
; APPLICANT: Ladner, Robert C.  
; APPLICANT: Arbogast, Christophe  
; APPLICANT: Busest, Philippe  
; APPLICANT: Pan, Hong Sudha  
; APPLICANT: Khurana, Linder, Karen E.

```

; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Machev A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-325

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Query Match      41.0%; Score 34; DB 1; Length 28;
Best Local Similarity 58.3%; Pred. No. 2;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy      5 IQLMHNLTGGGG 16
      || : |||
Db     15 IQRVDSLITGGGG 26

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Search completed: November 21, 2005, 16:56:34  
Job time : 6 secs

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